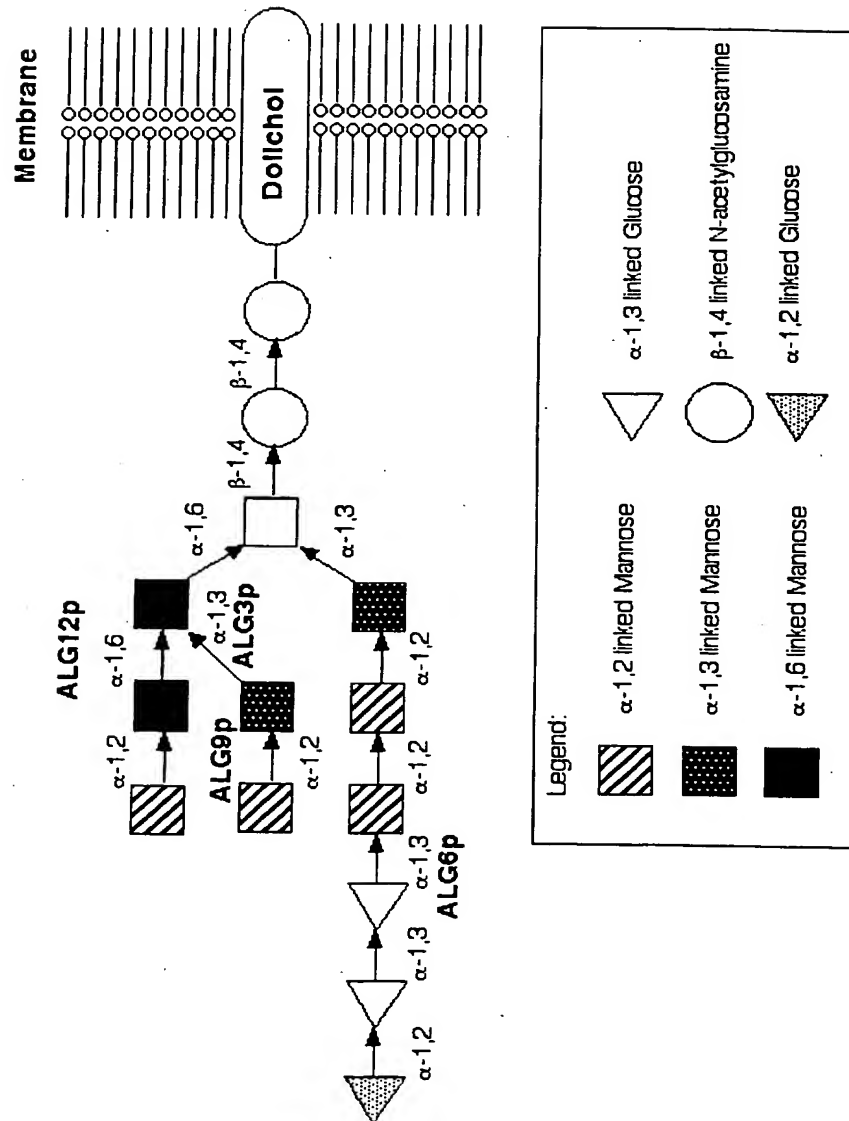


10/500240

FIGURE 1



## Lipid-linked N-glycans

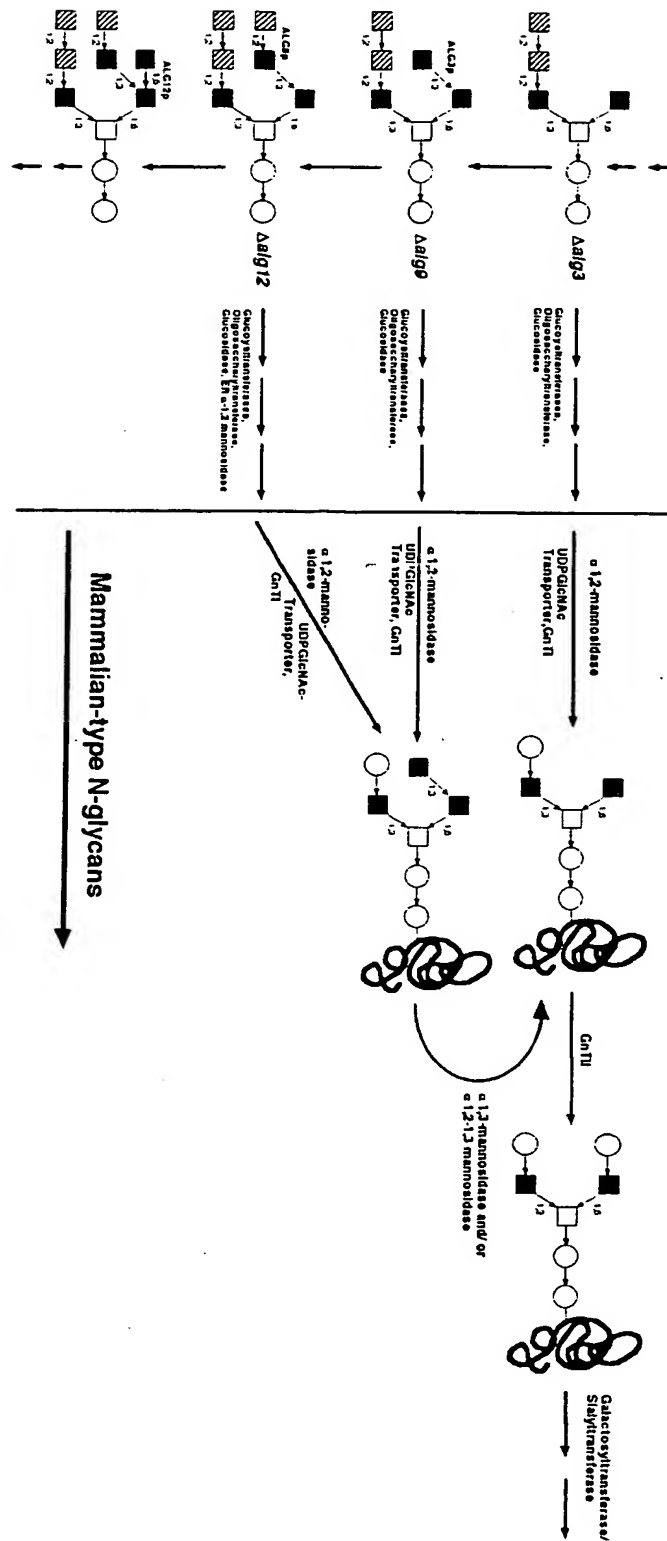


FIGURE 2

FIGURE 3

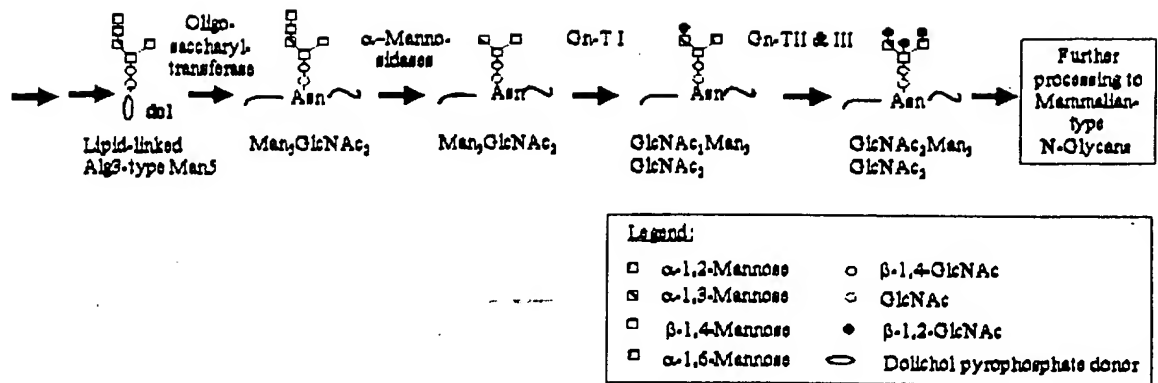


FIGURE 4 (sheet 1)

## ALG3 Blast 05-22-01

Sequences producing significant alignments: (bits) Value

gi 586444 sp P38179 ALG3_YEAST	DOLICHYL-P-MAN:MAN(5)GLCNAC(...797	0.0
gi 3024226 sp Q92685 ALG3_HUMAN	DOLICHYL-P-MAN:MAN(5)GLCNAC...173	7e-43
gi 3024221 sp Q24332 NT56_DROVI	LETHAL(2)NEIGHBOUR OF TID P...145	3e-34
gi 3024222 sp Q27333 NT56_DROME	LETHAL(2)NEIGHBOUR OF TID P...121	3e-27
gi 10720153 sp P82149 NT53_DROME	LETHAL(2)NEIGHBOUR OF TID ...121	5e-27
gi 1707982 sp P40989 GLS2_YEAST	1,3-BETA-GLUCAN SYNTHASE CO... 32	2.8
gi 1346146 sp P38631 GLS1_YEAST	1,3-BETA-GLUCAN SYNTHASE CO... 31	6.6

## Alignments

Yeast

>gi|586444|sp|P38179|ALG3\_YEAST DOLICHYL-P-MAN:MAN(5)GLCNAC(2)-PP-DOLICHYL MANNOSYLTRANSFERASE  
 (DOL-P-MAN DEPENDENT ALPHA(1-3)-MANNOSYLTRANSFERASE)  
 (HM-1 KILLER TOXIN RESISTANCE PROTEIN)  
 Length = 458

Score = 797 bits (2059), Expect = 0.0  
 Identities = 422/458 (92%), Positives = 422/458 (92%)

Query: 1	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYIFDCRANLIVMPLLILFESMLCKI	60
	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYIFDCRANLIVMPLLILFESMLCKI	
Sbjct: 1	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYIFDCRANLIVMPLLILFESMLCKI	60
Query: 61	IIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGM	120
	IIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGM	
Sbjct: 61	IIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGM	120
Query: 121	DHVERGQVFFRYLYLLTLALQMACYLLHLPWCVVLACLSKRLHSIYVLRFLNDCFTTL	180
	DHVERGQVFFRYLYLLTLALQMACYLLHLPWCVVLACLSKRLHSIYVLRFLNDCFTTL	
Sbjct: 121	DHVERGQVFFRYLYLLTLALQMACYLLHLPWCVVLACLSKRLHSIYVLRFLNDCFTTL	180
Query: 181	FMVVTVLGAIVASRCHORPKLKKSLALVISATYSMAVSIKMNALLYFPAMMISLFILNDA	240
	FMVVTVLGAIVASRCHORPKLKKSLALVISATYSMAVSIKMNALLYFPAMMISLFILNDA	
Sbjct: 181	FMVVTVLGAIVASRCHORPKLKKSLALVISATYSMAVSIKMNALLYFPAMMISLFILNDA	240
Query: 241	NVILTLLDLVAMIAWQVAVAVPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEAFND	300
	NVILTLLDLVAMIAWQVAVAVPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEAFND	
Sbjct: 241	NVILTLLDLVAMIAWQVAVAVPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEAFND	300
Query: 301	KRFXXXXXXXXXXXXXXXXFVTRYPRILPDLWSSLCHPLRKNAVLNANPAKTIPFVLIASN	360
	KRF FVTRYPRILPDLWSSLCHPLRKNAVLNANPAKTIPFVLIASN	
Sbjct: 301	KRFHLALLISHLIALTTLFVTRYPRILPDLWSSLCHPLRKNAVLNANPAKTIPFVLIASN	360
Query: 361	FIGVLFPSRLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLHEWCWNSYPPNSQXXXXX	420
	FIGVLFPSRLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLHEWCWNSYPPNSQ	
Sbjct: 361	FIGVLFPSRLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLHEWCWNSYPPNSQASTLL	420
Query: 421	XXXXXXXXXXXXXXXXXSGSVALAKSHLRTTSSMEKKLN	458
	SGSVALAKSHLRTTSSMEKKLN	
Sbjct: 421	LALNTVLLLLLALQLSGSVALAKSHLRTTSSMEKKLN	458

FIGURE 4 (sheet 2)

Human

>gi|3024226|sp|Q92685|ALG3\_HUMAN DOLICHYL-P-MAN:MAN(5)GLCNAC(2)-PP-DOLICHYL  
MANNOSYLTRANSFERASE

(DOL-P-MAN DEPENDENT ALPHA(1-3)-MANNOSYLTRANSFERASE)

(NOT56-LIKE PROTEIN)

Length = 438

Score = 173 bits (439), Expect = 7e-43

Identities = 133/396 (33%), Positives = 195/396 (48%), Gaps = 28/396 (7%)

Query: 26 WQDLKDGVRVIFDCRANLIVMPLLILFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLD 85  
WQ+ R++R L+V LLE + +I +VAYTEID+KAYM ++E + ++  
Sbjct: 29 WQER---RLLLREPRYTLLVAACLCLAEVGITFWVIHRVAYTEIDWKAYMAEVEGV-IN 83

Query: 86 GMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACY 145  
G DY+Q+ G TGPLVYPAG V I+ +Y+ T + Q F LYL TL L Y  
Sbjct: 84 GTYDYTQLQGDGTGPLVYPAGFVYIFMGLYYATSRGTDIRMAQNIFAVLYLATLLLVFLIY 143

Query: 146 Y-LLHLPWC-VVLACLSKRLHSIYVLRFLNDCFTTLFMVVTVLGAIVASRCHQRPKLKK 203  
+ +PP+ + C S R+HSI+VLRFLND + + +L + QR  
Sbjct: 144 HQTKVPPFVFFFMCCASYRVHSIFVLRFLNDP-----VAMVLLFLSINLLLAQRWGWG- 197

Query: 204 SLALVISATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPF 263  
+S+AVS+KMN LL+ P ++ L L L + A + QV + +PF  
Sbjct: 198 -----CCFFSLAVSVKMNVLFFAPGLLFLLLLTQFGFRGALPKLGICAGL--QVVLGLPF 249

Query: 264 LRSFPQQLHCAFNFRKFMYSINWQMMDEEAFNDKRFXXXXXXXXXXXXXXXXXFFVTRY 323  
L P YL +F+ GR+F++ W++NW+ + E F + F + R+  
Sbjct: 250 LLENPSGYLSRSFDLGRQFLFHWTVNWRFLPEALFLHRAFLALLTAHLTLLLLFALCRW 309

Query: 324 PRILPDLWSSLCHPLRKNVLANPAKTIPFVLIASNFIGVLFSRSLHYQFLSWYHWTLP 383  
R + S L P ++ I L SNFIG+ FSRSLHYQF WY TLP  
Sbjct: 310 HRTGESILSLLRDPSKRKVPPQPLTNQIVSTLFTSNFIGICFSRSLHYQFYVWYFHTLP 369

Query: 384 ILIF----WSGMPFFVGPIWYVLHEWCWNSYPPNS 414  
L++ W + + + E WN+YP S  
Sbjct: 370 YLLWAMPARWLTHLLRLLVLGLI--ELSWNTYPSTS 403

Drosophila Vi

>gi|3024221|sp|Q24332|NT56\_DROVI LETHAL(2)NEIGHBOUR OF TID PROTEIN (NOT58)  
Length = 526

Score = 145 bits (366), Expect = 3e-34

Identities = 103/273 (37%), Positives = 157/273 (56%), Gaps = 17/273 (6%)

Query: 33 VRYVIFDCRANLIVMPLLILFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQ 92  
++Y+ F+ A IV L++L E+++ ++I++V YTEID+KAYM++ E L+G +YS  
Sbjct: 34 IKYLAFEPAALPIVSVLIVLAEAVINVLVIRVPTYTEIDWKAYMQECEGF-LNGTTNYSL 92

Query: 93 VSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACYLLH-LP 151  
+ G TGPLVYPA V IY +Y+LT +V Q F +YLL + L + Y +P  
Sbjct: 93 LRGDTGPLVYPAAFVYIYSGLYLTGQGTNVRLAQYIFACIYLLQMCLVLRLYTKSRKVP 152

Query: 152 PWCVVLACL-SKRLHSIYVLRFLNDCFTTLFMVVTVLGAIVASRCHQRPKLKSLALVIS 210  
P+ +VL+ S R+HSIYVLRFLND L +L A + QR L S  
Sbjct: 153 PYVLVLSAFTSYRIHSIYVLRFLNDPVAAIL-----LLYAALNLFQDQRTLG-----S 200

Query: 211 ATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPFLRSFPQ 270  
YS+AV +KMN + A + LF L + V+ TL+ L Q+ + PFLR+ P +  
Sbjct: 201 ICYSLAVGVKMN--ILLFAPALLLFYLANLGVRLTLVQLTICAVLQLFIGAPFLRTHPME 258

FIGURE 4 (sheet 3)

Query: 271 YLHCAFNFGRKFMYQWSINWQMMDEEAFNDKRF 303  
 YL +F+ GR F ++W++N++ + +E F + F  
 Sbjct: 259 YLRGSFDLGRIFEHKWTVNYRFLSKELFEQREF 291

Score = 53.3 bits (127), Expect = 1e-06  
 Identities = 31/62 (50%), Positives = 41/62 (66%), Gaps = 6/62 (9%)

Query: 352 IPFVLIASNFIGVLFSSRLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLH--EWCWNS 409  
 +PF L NFIGV +RSLHYQF WY +LP L+ WS P+ +G + +L E+CWN+  
 Sbjct: 412 LPFFL--CNFIGVACARSRLHYQFYIWFHSLPYLV-WS-TPYSLGVRYLILGLIEYCWN 467

Query: 410 YP 411  
 YP  
 Sbjct: 468 YP 469

### Drosophila melanogaster

>gi|3024222|sp|Q27333|NT56\_DROME LETHAL(2)NEIGHBOUR OF TID PROTEIN (NOT56)  
 (NOT45)

Length = 510

Score = 121 bits (305), Expect = 3e-27  
 Identities = 96/272 (35%), Positives = 154/272 (56%), Gaps = 17/272 (6%)

Query: 34 RYVIFDCRANLIVMPLLLFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQV 93  
 +Y++ + A IV ++L E ++ ++I++V YTEID+ AYM++ E L+G +YS +  
 Sbjct: 36 KYLLLEPAALPIVGLFVLLAELVINVVVIQRPVYTEIDWVAYMQECEGF-LNGTTNYSLL 94

Query: 94 SGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGOVFFRYLYLLTLALQMACYLLH-LPP 152  
 G TGPLVYPA V IY +Y++T +V Q F +YLL LAL + Y +PP  
 Sbjct: 95 RGDTPGLVYPAAFVYIYSALYYVTSHGNTVRLAQYIFAGIYLLQLALVLRLYSKSRKVPP 154

Query: 153 WCVVLACL-SKRLHSIYVLRFLFNDCTTLFMVVTVLGAIVASRCHQRPKLKSLALVISA 211  
 + +VL+ S R+HSIYVLRFLFND + V +L A + +R L S  
 Sbjct: 155 YVLVLSAFTSYRIHSIYVLRFLFNDP-----VAVLLLYAALNLFDRRWTLG-----ST 202

Query: 212 TYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPFLRSFPQQY 271  
 +S+AV +KMN + A + LF L + ++ T+L L Q+ + PFL + P +Y  
 Sbjct: 203 FFSLAVGVKMN--ILLFAPALLLFYLANLGLLRTILQLAVCGVIQLLLGAPFLLTHPVEY 260

Query: 272 LHCAFNFGRKFMYQWSINWQMMDEEAFNDKRF 303  
 L +F+ GR F ++W++N++ + + F ++ F  
 Sbjct: 261 LRGSFDLGRIFEHKWTVNYRFLSRDVFENRTF 292

Score = 49.4 bits (117), Expect = 2e-05  
 Identities = 27/60 (45%), Positives = 35/60 (58%), Gaps = 2/60 (3%)

Query: 352 IPFVLIASNFIGVLFSSRLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLHEWCWNSYP 411  
 +PF L N +GV SRSLHYQF WY +LP L + + V + L E+CWN+YP  
 Sbjct: 407 LPFFL--CNLVGVACSRSLHYQFYVWFHSLPYLAWSTPYSLGVRCILGLIEYCWN 464

## FIGURE 4 (sheet 4)

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Hits to DB: 28883317  
Number of Sequences: 96469  
Number of extensions: 1107545  
Number of successful extensions: 2870  
Number of sequences better than 10.0: 16  
Number of HSP's better than 10.0 without gapping: 5  
Number of HSP's successfully gapped in prelim test: 11  
Number of HSP's that attempted gapping in prelim test: 2839  
Number of HSP's gapped (non-prelim): 23

length of query: 458  
length of database: 35,174,128  
effective HSP length: 45  
effective length of query: 413  
effective length of database: 30,833,023  
effective search space: 12734038499  
effective search space used: 12734038499  
T: 11  
A: 40  
X1: 15 ( 7.1 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 40 (21.8 bits)  
S2: 67 (30.4 bits)

FIGURE 5

*S. cerevisiae* ALG3

ATGGAAGGTGAACAGTCTCCGCAAGGTGAAAAGTCTCTGCAAAGGAAGC  
 AATTTGTCAGACCTCCGCTGGATCTGTGGCAGGATCTCAAGGACGGTGTG  
 CGCTACGTGATCTTCGATTGTAGGGCCAATCTTATCGTTATGCCCTTTTG  
 ATTTTGTTCGAAAGCATGCTGTGCAAGATTATCATTAAAGAAGGTAGCTTAC  
 ACAGAGATCGATTACAAGGCGTACATGGAGCAGATCGAGATGATTCAGCT  
 CGATGGCATGCTGGACTACTCTCAGGTGAGTGGTGGAACGGGGCCCGCTGG  
 TGTATCCAGCAGGCCACGTCTTGATCTACAAGATGATGTACTGGCTAACA  
 GAGGGAATGGACCACGTTGAGCGCGGGCAAGTGTTTTTCAGATACTTGTA  
 TCTCCTTACACTGGCGTTACAAATGGCGTGTTACTACCTTTTACATCTACC  
 ACCGTGGTGTGTGGTCTTGGCGTGCCTCTCTAAAAGATTGCACTCTATTTA  
 CGTGCTACGGTTATTCAATGATTGCTTCACTACTTTGTTTATGGTCGTCACG  
 GTTTTGGGGGCTATCGTGGCCAGCAGGTGCCATCAGCGCCCCAAATTTAA  
 GAAGTCCCTTGCGCTGGTGTATCTCCGCAACATACAGTATGGCTGTGAGCA  
 TTAAGATGAATGCGCTGTTGTATTTCCCTGCAATGATGATTTCTCTATTTCAT  
 CCTTAATGACGCGAACGTAATCCTTACTTTGTTGGATCTCGTTGCGATGAT  
 TGCATGGCAAGTCGCAGTTGCAGTGCCCTTCTGCGCAGCTTTCCGCAACA  
 GTACCTGCATTGCGCTTTTAATTTTCGGCAGGAAGTTTATGTACCAATGGAG  
 TATCAATTGGCAAATGATGGATGAAGAGGCTTTCAATGATAAGAGGTTCC  
 ACTTGGCCCTTTTAATCAGCCACCTGATAGCGCTCACCACACTGTTTCGTCA  
 CAAGATACCCTCGCATCCTGCCCCGATTTATGGTCTTCCCTGTGCCATCCGC  
 TGAGGAAAAATGCAGTGCTCAATGCCAATCCCGCCAAGACTATTCCATTC  
 GTTCTAATCGCATCCAACCTTCATCGGCGTCCTATTTTCAAGGTCCCTCCAC  
 TACCAGTTTCTATCCTGGTATCACTGGACTTTGCCTATACTGATCTTTTGGT  
 CGGGAATGCCCTTCTTCGTTGGTCCCATTTGGTACGTCTTGCACGAGTGGT  
 GCTGGAATTCTATCCACCAAACTCACAAGCAAGCACGCTATTGTTGGCA  
 TTGAATACTGTTCTGTTGCTTCTATTGGCCTTGACGCAGCTATCTGGTTCGG  
 TCGCCCTCGCCAAAAGCCATCTTCGTACCACCAGCTCTATGGAAAAAAG  
 CTCAACTGA

*S. cerevisiae* Alg3p

MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYVIFDCRANLIVMPLLIL  
 FESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGM LDYSQVSGGTGPLVYPAG  
 HVLIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACYLLHLPPWCV  
 VLACLSKRLHSIYVLRLFNDCFTTLFMVVTVLGAIVASRCHQRPKLKKSALV  
 ISATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVA  
 VPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEAFNDKRFHLALLISHL  
 IALTTLFVTRYPRILPDLWSSLCHPLRKNVNLNANPAKTIPFVLIASNFIGVLFS  
 RSLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLHEWCWNSYPPNSQASTL  
 LLALNTVLLLLLALTQLSGSVALAKSHLRTTSSMEKKLN



FIGURE 6

*P. pastoris* ALG3

ATGCCTCCGATAGAGCCAGCTGAAAGGCCAAAGCTTACGCTGAAAAATGT  
 TATCGGTGATCTAGTGGCTCTTATTCAAACGTTTTATTAAACCCAGATTTT  
 AGTGTCTTCGTTGCACCTCTTTTATGGTTAGCTGATTCCATTGTTATCAAGG  
 TGATCATTGGCACTGTTTCCTACACAGATATTGATTTTTCTTCATATATGCA  
 ACAAATCTTTAAAATTTCGACAAGGAGAATTAGATTATAGCAACATATTTG  
 GTGACACCGGTCCATTGGTTTACCCAGCCGGCCATGTTTCATGCTTACTCAG  
 TACTTTTCGTGGTACAGTGATGGTGGAGAAGACGTCAGTTTCGTTCAACAA  
 GCATTTGGTTGGTTATACCTAGGTTGCTTGTTACTATCCATCAGCTCCTACT  
 TTTTCTCTGGCTTAGGGAAAATACCTCCGGTTTATTTTGTTTTGTTGGTAGC  
 GTCCAAGAGACTGCATTCAATATTTGTATTGAGACTCTTCAATGACTGTTT  
 AACAAACATTTTTGATGTTGGCAACTATAATCATCCTTCAACAAGCAAGTAG  
 CTGGAGGAAAGATGGCACAACCTATTCATTATCTGTCCCTGATGCTGCAG  
 ATACGTACAGTTTAGCCATCTCTGTAAAGATGAATGCGCTGCTATACCTCC  
 CAGCATTCCCTACTACTCATATATCTCATTGTGACGAAAATTTGATTAAAG  
 CCTTGGCACCTGTTCTAGTTTTGATATTGGTGCAAGTAGGAGTCGGTTATT  
 CGTTCATTTTACCGTTGCACTATGATGATCAGGCAAATGAAATTCGTTCTG  
 CCTACTTTAGACAGGCTTTTGACTTTAGTCGCCAATTTCTTTATAAGTGGA  
 CGGTTAATTGGCGCTTTTTGAGCCAAGAACTTTCAACAATGTCCATTTTC  
 ACCAGCTCCTGTTTGCTCTCCATATTATTACGTTAGTCTTGTTTCATCCTCAA  
 GTTCCTCTCTCCTAAAAACATTGGAACCGCTTGGTAGATTTGTGTTGGA  
 CATTTTCAAATTTTGGAAAGCCAACCTTATCTCCAACCAATATTATCAACGA  
 CCCAGAAAGAAGCCCAGATTTTGTTTACACCGTCATGGCTACTACCAACTT  
 AATAGGGGTGCTTTTTGCAAGATCTTTACACTACCAGTTCCTAAGCTGGTA  
 TCGGTTCTCTTTGCCATATCTCCTTTACAAGGCTCGTCTGAACTTTATAGCA  
 TCTATTATTGTTTATGCCGCTCACGAGTATTGCTGGTTGGTTTTCCAGCTA  
 CAGAACAAAGTTCCGCGTTGTTGGTATCTATCTTACTACTTATCCTGATTC  
 TCATTTTTACCAACGAACAGTTATTTCTTCTCAATCGGTCCCTGCAGAAA  
 AAAAGAATACATAA

*P. pastoris* Alg3p

MPPIEPAERPRLTLKNVIGDLVALIQNVLFNPDFS VFVAPLLWLADSIVIKVIIG  
 TVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAYSVLSWYS  
 DGGEDVSFVQQAAGWLYLGCLLSISSYFFSGLGKIPPVYFVLLVASKRLHSIF  
 VLRLFNDCLTTFMLLATIHLQQASSWRKDGTTIPLSVPDAADTYSLAISVKMN  
 ALLYLPAFLLLIYLICDENLIKALAPVLVLILVQVGVGYSFILPLHYDDQANEIR  
 SAYFRQAFDFSQRQFLYKWTNVNRFLSQETFNNVHFHQLLFALHIITLVLFILKF  
 LSPKNIGKPLGRFVLDIFKFWKPTLSPTNIINDPERSPDFVYTVMATTNLIGVLF  
 ARSLHYQFLSWYAFSLPYLLYKARLNFIASIIVYAAHEYCWLVPATEQSSAL  
 LVSILLILILIFTNEQLFPSQSVPAEKKNT

FIGURE 7 (sheet 1)

*P. pastoris* ALG3 BLAST

Sequences producing significant alignments: (bits) Value

gi 586444 sp P38179 ALG3 YEAST Dolichyl-P-Man:Man(5)GlcNAc(...228	2e-58
gi 12802365 gb AAK07848.1 AF309689.10 putative NOT-56 manno...212	8e-54
gi 984725 gb AAA75352.1  ORF 1 206	4e-52
gi 7492702 pir T39084 probable mannosyltransferase - fissi...176	8e-43
gi 16226531 gb AAL16193.1 AF428424.1 At2g47760/F17A22.15 [A...164	2e-39
gi 25367230 pir B84919 Not56-like protein [imported] - Ara...164	3e-39
gi 25814791 emb CAB70171.2  Hypothetical protein K09E4.2 [C...161	2e-38
gi 17535001 ref NP_496950.1  Putative plasma membrane membr...160	3e-38
gi 1654000 emb CAA70220.1  Not56-like protein [Homo sapiens...155	2e-36
gi 13279206 gb AAH04313.1 AAH04313 Unknown (protein for IMA...154	2e-36
gi 22122365 ref NP_666051.1  hypothetical protein MGC36684 ...150	3e-35
gi 21292031 gb EAA04176.1  agCP3388 [Anopheles gambiae str....120	4e-26
gi 1780792 emb CAA71167.1  lethal(2)neighbour of tid [Droso...114	3e-24

## Alignments

*S. cerevisiae*

Score = 228 bits (580), Expect = 2e-58

Identities = 154/429 (35%), Positives = 229/429 (53%), Gaps = 37/429 (8%)

Query: 9 RPKLTLKNVIGDLVALIQNVLFNPDFSVFVAPLLWLADSIIVIKVIIGTVSYTDIDFSSYM 68  
 RP L L DL ++ V+F+ ++ V PLL L +S++ K+II V+YT+ID+ +YM  
 Sbjct: 20 RPPLDLWQ---DLKDGVRVYIFDCRANLIVMPLLILFESMLCKIIKKVAYTEIDYKAYM 76

Query: 69 QQIFKIR-QGELDYSNIFGDTGPLVYPAGHVHAYSVLSWYSDGGEDVSFVQQAAGWLYLG 127  
 +QI I+ G LDYS + G TGPLVYPAGHV Y ++ W ++G + V Q F +LYL  
 Sbjct: 77 EQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLL 136

Query: 128 CLLLSISSYFFSGLGKIPPVYFVLLVASKRLHSIFVLRLFNDCLTTFMLLATI---IILQ 184  
 L L ++ Y+ L +PP VL SKRLHSI+VLRLFNDC TT M+ T+ I+  
 Sbjct: 137 TLALQMACYY---LLHLPWCVVLAACLSKRLHSIYVLRLFNDCFTTLFMVVTVLGAIVAS 193

Query: 185 QASSWRKDGTTIPLSVPDAADTYSLAISVKMNXNXXXXXXXXXXXXXXXXXCDENLIKALAPXX 244  
 + K ++ L + + TYS+A+S+KMN D N+I L  
 Sbjct: 194 RCHQRPKLKSLALVI---SATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLV 250

Query: 245 XXXXXXXXXXXYSFILPLHYDDQANEIRSAYFRQAFDFSRQFLYKWTVNWRFLSQETFNNV 304  
 F+ Y AF+F R+F+Y+W++NW+ + +E FN+  
 Sbjct: 251 AMIAWQVAVAVPFL-----RSFPQQLHCAFNFRKFMYSINWQMMDEEAFNDK 301

Query: 305 HFHQLLFALHIITL-VLFILKFLSPKNIGKPLGRFVLDIFKFWKPTLSPTNIIN-DPERS 362  
 FH L H+I L LF+ ++ R + D++ L ++N +P ++  
 Sbjct: 302 RFHLALLISHLIALTTLVTRY-----PRILPDLWSSLCHPLRKNVLANPNAKT 351

Query: 363 PDFVYTVMATTNLIGVLFARSLHYQFLSWYAFSLPYLLYKARLNFIASIIVYAAHEYCWL 422  
 F V+ +N IGVLF+RSLHYQFLSWY ++LP L++ + + F I Y HE+CW  
 Sbjct: 352 IPF---VLIASNFIGVLFARSRLHYQFLSWYHTLPILIFWSGMPFFVGPIWYVLHEWCWN 408

Query: 423 VFPATEQSS 431  
 +P Q+S  
 Sbjct: 409 SYPPNSQAS 417

FIGURE 7 (sheet 2)

*Neurospora crassa*

Score = 212 bits (540), Expect = 8e-54

Identities = 140/400 (35%), Positives = 212/400 (53%), Gaps = 29/400 (7%)

Query: 35 SVFVAPLLWLADSIVIKVIIGTVSYTDIDFSSYMQIFKIROGELDYSNIFGDTGPLVYP 94  
S + P L+L D+++ +II V YT+ID+++YM+Q+ +I GE DY+ + G TGPLVYP

Sbjct: 33 SKLIPPALFLVDALLCGLIIVKVPYTEIDWAAAYEQVSQILSGERDYTKVRGGTGPLVYP 92

Query: 95 AGHVHAYSVLSWYSDGGEDVSFVQQAAGWLYLGCLLLSISSYFFSGLGKIPPVYFVLLVA 154  
A HV+ Y+ L +D G ++ QQ F LY+ L + + Y+ K PP F LL

Sbjct: 93 AAHVYIYTGLYHLTDEGRNILLAQQLFAGLYMVT LAVVMGCYW---QAKAPPYLFPLLTL 149

Query: 155 SKRLHSIFVLRFNDC + I Q+ +W+ A Y+L + VK 214  
SKRLHSIFVLR FNDC + I Q+ +W+ A Y+L + VK

Sbjct: 150 SKRLHSIFVLRFCFNDCFAVLFWLAIFFQFQ-RNWQA-----GALLYTLGLGVK 197

Query: 215 MNXXXXXXXXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXSYFILPLHYDDQANEIRSAY 274  
M + + L F+ HY + Y

Sbjct: 198 MTLTLLSLPAVGIVLFLGSG-SFVTTLQLVATMGLVQILIGVPFL--AHYPT-----Y 247

Query: 275 FRQAFDFSROFLYKWTNVNRFSLQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGK 333  
+AF+ SRQF +KWTNVNRF+ +E F + "F" L ALH++ L +FI +++ P K

Sbjct: 248 LSRAFELSRQFFFKWTNVNRFVGEIEFLSKGFALTLLALHVLVLGIFITTRWIKPAR--K 305

Query: 334 PLGRFVLDFKFWKPTLS-PTNIINDPERSPDFVYTMATTNLIGVLFARSLHYQFLSWY 392  
L + + + KP L+ P + +P ++ T + + N +G+LFARSLHYQF ++

Sbjct: 306 SLVQLISPVLLAGKPPLTVPEHRAAARDVTPRYIMTTILSANAVGLLFAARSLHYQFYAYV 365

Query: 393 AFSLPYLLYKARLNFIAIIIVYAAHEYCWLVFPATEQSSA 432  
A+S P+LL++A L+ + +++A HE+ W VFP+T SSA

Sbjct: 366 AWSTPFLLRAGLHPVLVYLLWAVHEWAWNVFPSTPASSA 405

*Schizosaccharomyces pombe*

Score = 176 bits (445), Expect = 8e-43

Identities = 132/390 (33%), Positives = 194/390 (49%), Gaps = 35/390 (8%)

Query: 42 LWLADSIVIKVIIGTVSYTDIDFSSYMQIFKIROGELDYSNIFGDTGPLVYPAGHVHAY 101  
L L + + II V YT+ID+ +YM+Q+ GE DY ++ G TGPLVYP GHV Y

Sbjct: 30 LLLLEIPFVFAIISKVPYTEIDWIAAYEQVNSFLLGERDYKSLVGCTGPLVYPGGHVFLY 89

Query: 102 SVLSWYSDGGEDVSFVQQAAGWLYLGCLLLSISSYFFSGLGKIPPVYFVLLVASKRLHSI 161  
++L + +DGG ++ Q F ++Y + +I Y F + + P +VLL+ SKRLHSI

Sbjct: 90 TLLYYLTDGGTNIVRAQYIFAFVYW--ITTAIVGYLFK-IVRAPFYIYVLLILSKRLHSI 146

Query: 162 FVLRFLNDCLTTFMLLATIIILQASSWRKDGTTIPLSVPAADTYSLAISVKMNXNXX 221  
F+LRLFNDC + L + I+ W + A+ S+A SVKM+

Sbjct: 147 FILRFLNDCGFNS-LFSSLFILSSCKKKWVR-----ASILLSVACSVKMSSLLYV 194

Query: 222 XXXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXSYFILPLHYDDQANEIRSAYFRQAFDF 281  
L++ L P + + + +Y+ QAFDF

Sbjct: 195 PAYLVL-----LLQILGPKKTWMHIFVIIIVQILFSIPF----LAYFWSYWTQAFDF 242

Query: 282 SRQFLYKWTNVNRFSLQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGKPLGRFVLD 341  
R F YKWTNVNRF+ + F + F + LH+ LV F K + + P

Sbjct: 243 GRAFDYKWTNVNRFIPRSIFESTSFSTSILFLHVALVAFTCKHWNKLSRATP----- 295

Query: 342 IFKFWKPTLSPTNIINDPERSPDFVYTMATTNLIGVLFARSLHYQFLSWYAFSLPYLLY 401  
F L+ + +P+F++T.+AT+NLIG+L ARSLHYQF +W+A+ PYL Y

## FIGURE 7 (sheet 3)

Sbjct: 296 -FAMVNSMLTLKPLPKLQLATPNFIFTALATSNLIGILCARSLHYQFYAWFAWYSPYLCY 354

Query: 402 KARLNFIASIIIVYAAHEYCWLVFPATEQSS 431  
 +A I ++ EY W VFP+T+ SS

Sbjct: 355 QASFPAPIVIGLWMLQEYAWNVPSTKLSS 384  
*Arabidopsis thaliana*

Score = 164 bits (415), Expect = 2e-39  
 Identities = 131/391 (33%), Positives = 194/391 (49%), Gaps = 29/391 (7%)

Query: 42 LWLADSIIVIKVIIGTVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAY 101  
 L LAD+I++ +II V YT ID+ +YM Q+ GE DY N+ GDTGPLVYPAG ++ Y

Sbjct: 39 LILADAILVALIIAYVPYTKIDWDAYMSQVSGFLGGERDYGNLKGGDTGPLVYPAGFLYVY 98

Query: 102 SVLSWYSDDGGEDVSFVQQAFGWLYLGCLLSISSYFFSGLGKIPPVYFVLLVASKRLHSI 161  
 S + + G +V Q FG LY+ L + + Y + + +P LL SKR+HSI

Sbjct: 99 SAVQNLTGG--EVYPAQILFGVLYIVNLGIVLIIYVKTDV--VPWWALSLLCLSKRIHSI 154

Query: 162 FVLRLFNDCLTTFMLLATIIILQQASSWRKDGTTIPLSVDAADTYSLAISVKMNXXXXX 221  
 FVLRLFNDC L+ A++ + +RK + + +S A+SVKMN

Sbjct: 155 FVLRLFNDCFAMTLLHASMALFL----YRKWHLGMLV-----FSGAVSVKMNVLLEYA 202

Query: 222 XXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXSYFILPLHYDDQANEIRSAYFRQAFDF 281  
 N+I ++ F++ +Y AFD

Sbjct: 203 PTLLLLLLKAM--NIIGVVSALAGAALAQILVGLPFLITYPV-----SYIANAFDL 251

Query: 282 SRQFLYKWTNVNRFLSQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGKPLGRFVLD 341  
 R F++ W+VN++F+ + F + F L H+ LV F + K+ G +G

Sbjct: 252 GRVFIHFWSVNFKFVPERVFSKEFAVCLLIAHLFLLVAFA-NYKWCKHEGGIIGFMRSR 310

Query: 342 IFKFWKP-TLSPTNIINDPERSPDFVYTMATTNIGVLFARSLHYQFLSWYAFSLPYLL 400  
 F P +LS +++ + + V T M N IG++FARSLHYQF SWY +SLPYLL

Sbjct: 311 HFFLTLPSSLSFSDVSASRIITKEHVVTAMFVGNFIVFARSLHYQFYSWYFYSLPYLL 370

Query: 401 YKARLNFIASIIIVYAAHEYCWLVFPATEQSS 431  
 ++ +I++ E CW V+P+T SS

Sbjct: 371 WRTPFPTWLRRLIMFLGIELCWNVPSTPSSS 401

FIGURE 8

*K. lactis* ALG3

TTTGTTTACAAGCTGATACCAACGAACATGAATACACCGGCAGGTTTACT  
GAAGATTGGCAAAGCTAACCTTTTACATCCTTTTACCGATGCTGTATTCAG  
TGCGATGAGAGTAAACGCAGAACAAATTGCATACATTTTACTTGTTACCA  
ATTACATTGGAGTACTATTTGCTCGATCATTACACTACCAATTCCTATCTT  
GGTACCATTGGACGTTACCAGTACTATTGAATTGGGCCAATGTTCCGTATC  
CGCTATGTGTGCTATGGTACCTAACACATGAGTGGTGCTGGAACAGCTAT  
CCGCCAAACGCTACTGCATCCACACTGCTACACGCGTGTAACACATACTG  
TTATTGGCTGTATTCTTAAGAGGACCCGCAAACCTCGAAAAGTGGTGATAA  
CGAAACAACACACGAGAAAGCTGAG

*K. lactis* Alg3p

FVYKLIPTNMNTPAGLLKIGKANLLHPFTDAVFSAMRVNAEQIAYILLVTNYI  
GVLFARSLHYQFLSWYHWTLPLVLLNWANVPYPLCVLWYLTHEWCWNSYPP  
NATASTLLHACNTYCYWLYSZEDPQTRKVVITKQHTRKL

FIGURE 9

*K. lactis* ALG3 BLAST

Score E  
Sequences producing significant alignments: (bits) Value

gi 586444 sp P38179 ALG3 YEAST	Dolichyl-P-Man:Man(5)GlcNAc(...)	125	1e-28
gi 984725 gb AAA75352.1	ORF 1	94	4e-19
gi 16226531 gb AAL16193.1	AF428424.1 At2g47760/F17A22.15 {A...	72	1e-12
gi 25367230 pir B84919	Not56-like protein [imported] - Ara...	72	1e-12
gi 21292031 gb EAA04176.1	agCP3388 [Anopheles gambiae str....]	69	2e-11
gi 20892051 ref XP_148657.1	similar to Lethal(2)neighbour ...	65	2e-10

## Alignments

*S. cerevisiae*

Score = 125 bits (314), Expect = 1e-28  
Identities = 60/120 (50%), Positives = 83/120 (69%), Gaps = 1/120 (0%)  
Frame = +3

Query: 66 ANLLHPFT-DAVFSAMRVNAEQIAYILLVTNYIGVLFARSLHYQFLSWYHWTLPVLLNWA 242  
++L HP +AV +A A+ I ++L+ +N+IGVLF+RSLHYQFLSWYHWTLP+L+ W+  
Sbjct: 332 SSLCHPLRKNVAVLNANP--AKTIPFVLIASNFIGVLFSSRSLHYQFLSWYHWTLPILIFWS 389

Query: 243 NVPYPLCVLWYLTHEWCWNSYPPNATASTLLHACNTYCYWLYS\*EDPQTRKVVITKQHTR 422  
+P+ + +WY+ HEWCWNSYPPN+ ASTLL A NT L + + V + K H R  
Sbjct: 390 GMPFFVGPIWYVLHEWCWNSYPPNSQASTLLALNTVLLLLLA-LTQLSGSVALAKSHLR 448

*A. thaliana*

Score = 72.0 bits (175), Expect = 1e-12  
Identities = 42/107 (39%), Positives = 57/107 (53%), Gaps = 3/107 (2%)  
Frame = +3

Query: 84 FTDVAVFSAMRVNAEQIAYILLVTNYIGVLFARSLHYQFLSWYHWTLPVLLNWANVPYPLC 263  
F+D S + + E + + V N+IG++FARSLHYQF SWY ++LP LL P L  
Sbjct: 322 FSDVSASRI-ITKEHVVTAMFVGNGFIGIVFARSLHYQFYSWYFYSLLPYLLWRTPFPTWLR 380

Query: 264 VLWYLTHEWCWNSYPPNATASTL---LHACNTYCYWLYS\*EDPQTRK 395  
++ +L E CWN YP ++S L LH WL DP K  
Sbjct: 381 LIMFLGIELCWNVYPSTPSSSGLLLCLHLIILVGLWLAPSVDPYQLK 427

FIGURE 10

*S. cerevisiae* ALG9

ATGAATTGCAAGGCGGTAACCATTAGTTTATTACTGTTGTTATTTTTAACAAGAGT  
 ATATATTCAGCCGACATTCTCGTTAATTTTCAGATTGCGATGAAACTTTTAATTATT  
 GGGAACCATTAAATTTATTGGTACGTGGATTGTTGTAACAAACCTGGGAATATTC  
 ACCCGAGTATTCTATTAGATCATGGGCTTTCTTATTACCTTTTTACTGTATTCTTTA  
 TCCAGTAAACAAATTTACTGACCTAGAAAGTCATTGGAACCTTTTTCATCACAAGA  
 GCATGCTTAGGCTTTTTTAGTTTTATCATGGAATTTAAACTACATCGTGAAATTGC  
 AGGCAGCTTGGCATTGCAAATCGCAAATATTTGGATTATTTTCCAATTGTTTAATC  
 CGGGCTGGTTCCATGCATCTGTGGAATTATTGCCTTCTGCCGTTGCCATGTTGTTG  
 TATGTAGGTGCCACCAGACACTCTCTACGCTATCTGTCCACTGGGTCTACTTCTAA  
 CTTTACGAAAAGTTTAGCGTACAATTTCTGGCTAGTATACTAGGCTGGCCATTTG  
 TTTTAATTTTAAGCTTGCCATTATGTTTACATTACCTTTTCAACCATAGAATTATTT  
 CTACCATCAGAACCGCATTTCGACTGCTGTTTGATATTTTCATTGACTGCATTTGCT  
 GTGATTGTCACTGACAGTATATTTTACGGGAAGCTTGCTCCTGTATCATGGAACA  
 TCTTATTTTACAATGTCATTAATGCAAGTGAGGAATCTGGCCCAAATATTTTCGGG  
 GTTGAGCCATGGTACTACTATCCACTAAATTTGTTACTGAATTTCCCACTGCCTGT  
 GCTAGTTTTAGCTATTTTGGGAATTTTCCATTTGAGATTATGGCCATTATGGGCAT  
 CATTATTCACATGGATTGCCGTTTTCACTCAACAACCTCACAAAGAGGAAAAGATT  
 TCTCTATCCAATTTACGGGTTAATAACTTTGAGTGCAAGTATCGCCTTTTACAAAG  
 TGTTGAATCTATTCAATAGAAAAGCCGATTCTTAAAAAAGGTATAAAGTTGTCAGT  
 TTTATTAATTGTTGCAGGCCAGGCAATGTCACGGATAGTGGCTTTGGTGAACAAT  
 TACACAGCTCCTATAGCCGTCTACGAGCAATTTTCTTCACTAAATCAAGGTGGTG  
 TGAAGGCACCGGTAGTGAATGTATGTACGGGACGTGAATGGTATCACTTCCCAAG  
 TTCTTTTCTGCTGCCAGATAATCATAGGCTAAAATTTGTTAAATCTGGATTTGATG  
 GTCTTCTTCCAGGTGATTTTCCAGAGAGTGGTTCTATTTTCAAAAAGATTAGAAT  
 TTACCTAAGGGAATGAATAACAAGAATATATATGATACCGGTAAAGAGTGGCCG  
 ATCACTAGATGTGATTATTTTATTGACATCGTCGCCCAATAAATTTAACAAAAG  
 ACGTTTTCAACCCTCTACATCTGATGGATAACTGGAATAAGCTGGCATGTGCTGC  
 ATTCATCGACGGTGAAAATTCTAAGATTTTGGGTAGAGCATTTTACGTACCGGAG  
 CCAATCAACCGAATCATGCAAATAGTTTACCAAAAACAATGGAATCAAGTGTACG  
 GTGTTTCGTTACATTGATTACTGTTTGTGTTGAAAAACCAACTGAGACTACTAATTGA

*S. cerevisiae* Alg9p

MNCKAVTISLLLLLFLTRVYIQPTFSLISDCDETFNYWEPLNLLVRGFGKQTWEYSPE  
 YSIRSWAFLLPFYCILYPVNKFTDLESHWNFFITRACLGFFSFIMEFKLHREIAGSLALQ  
 IANIWIIFQLFNPWFHASVELLPASVAMLLYVGATRHSLRYLSTGSTSNFTKSLAYN  
 FLASILGWPFVLILSLPLCLHYLFNHRHISTIRTAFCCLIFSLTAFVIVTDSIFYGKLAP  
 VSWNILFYNVINASEESGPNIFGVEPWYYPYPLNLLNFPLPVLVLAAILGIFHLRLWPLW  
 ASLFTWIAVFTQQPHKEERFLYPIYGLITLSASIAFYKVLNLFNRKPILKKGIKLSVLLI  
 VAGQAMSRIVALVNNYTAPIAVVEQFSSLNQGGVKAPVVNVCTGREWYHFPSSFLLP  
 DNHRLKFVKSFGDGLLPDGFPESGSIFKKIRTLPGKGMNNKNIYDTGKEWPITRCDYFI  
 DIVAPINLTKDVFNPLHLMDNWNKLACAAAFIDGENSKILGRAFYVPEPINRIMQIVLP  
 KQWNQVYGVRYIDYCLFEKPTETTN

**FIGURE 11**

*P. pastoris* ALG9

TGGCCTTCCTGTCTGCTCGATACTTCCTTTTACAGTAACCAACATACATGTT  
CTCCAACATGCTCTTGTATGTATTGGCCTATTCTATCTTGAGACTTGATATC  
AACCTTCTATGGTATTATTTTCAGACTGTGATGAAGTGTTCAACTACTGGGA  
GCCACTCAACTTCATGCTTAGAGGGTTTGGAAAACAGACTTGGGAGTATT  
CTCCAGAGTATGCCATCCGATCTTGGTCCTATCTAGTGCCACTTTGGATAG  
CAGGCTATCCACCATTGTTCCCTGGATATCCCTTCTTACTACTTTTTCTACTT  
TTTCAGACTACTGCTGGTTATTTTTTTCATTGGTTGCAGAAGTCAAGTTGTA  
CCATAGTTTGAAGAAAAATGTCAGCAGTAAGATCAGTTTCTGGTACCTTCT  
ATTTACAACCGTTGCTCCAGGAATGTCTCATAGCACGATAGCCTTATTACC  
ATCCTCTTTTGCTATGGTTTGTACACTTTTGCCATTAGATACGTCATTGAT  
TACCTACAATTACCAACATTAATGCGCACAATCAGAGAGACTGCTGCCAT  
CTCACCAGCTCACAAACAACAACACTAGCCAACTCTCTC

*P. pastoris* Alg9p

WPSCLLDTSFYSNQHTCSPTCSCMYWPILSZDLISTFYGIISDCDEVFNYWEPL  
NFMLRGFGKQTWEYSPEYAIRSWSYLVPLWLAGYPPLFLDIPSYFFFYFFRLLL  
VIFSLVAEVKLYHSLKKNVSSKISFWYLLFTTVAPGMSHSTIALLPSSFAMVCH  
TFAIRYVIDYLQLPTLMRTIRETAAISPAHKQQLANSL



FIGURE 12 (sheet 1)

*P. pastoris* ALG9 BLAST

Score E  
Sequences producing significant alignments: (bits) Value

gi 6324110 ref NP_014180.1	catalyzes the transfer of manno...	131	1e-29
gi 21296668 gb EAA08813.1	agCP7810 [Anopheles gambiae str....]	110	2e-23
gi 7019765 emb CAB75773.1	putative mannosyltransferase inv...	104	1e-21
gi 26341066 dbj BAC34195.1	unnamed protein product [Mus mu...	99	4e-20
gi 16551378 gb AAL25798.1	DIBD1 [Homo sapiens]	99	4e-20
gi 19527202 ref NP_598742.1	RIKEN cDNA 8230402H15 [Mus mus...	99	4e-20
gi 12053349 emb CAB66861.1	hypothetical protein [Homo sapi...	99	4e-20

## Alignments

*S. cerevisiae*

Score = 131 bits (329), Expect = 1e-29  
Identities = 62/141 (43%), Positives = 91/141 (64%), Gaps = 1/141 (0%)  
Frame = +2

Query: 200 ISTFYGIISDCDEVFNWYWEPLNFMRLRGFGKQTWEYSPEYAIRSWSYLVPLWIAGYP-PLF 376  
I + +ISDCDE FNYWEPLN ++RGFGKQTWEYSPEY+IRSW++L+P + YP F  
Sbjct: 21 IQPTFSLISDCDETFFNYWEPLNLLVRGFGKQTWEYSPEYSIRSWAFLLPFYICILYPVNKF 80

Query: 377 LDIPSXXXXXXXXRLLLVIFSLVAEVKLYHSLKKNVSSKISFWYLLFTTVAPGMSHSTIAL 556  
D+ S R L FS + E KL+ + +++ +I+ +++F PG H+++ L  
Sbjct: 81 TDLESHWNFFITRACLGFFSFIMEFKLHREIAGSLALQIANIWIIFQLFNPGWFWHASVEL 140

Query: 557 LPSSFAMVCHTFAIRYVIDYL 619  
LPS+ AM+ + A R+ + YL  
Sbjct: 141 LPSAVAMLLYVGATRHSLRYL 161

*Anopheles gambiae*

Score = 110 bits (274), Expect = 2e-23  
Identities = 58/130 (44%), Positives = 79/130 (60%), Gaps = 3/130 (2%)  
Frame = +2

Query: 197 LISTFYGIISDCDEVFNWYWEPLNFMRLRGFGKQTWEYSPEYAIRSWSYLVPLWIAGYPPLF 376  
L S Y IISDCDE +NYWEPL+++L+G G QTWEYSPE+A+RS+SY LW+ G P  
Sbjct: 34 LQSALYSIISDCDETFFNYWEPLHYLLKKGFGQTWEYSPEFALRSYSY---LWLHGLPAKV 90

Query: 377 LDIPS---XXXXXXXXRLLLVIFSLVAEVKLYHSLKKNVSSKISFWYLLFTTVAPGMSHST 547  
L + + R LL + + E +LY L + ++ +LLF + GM S+  
Sbjct: 91 LQLMTDNGVLIFYFVRCLLAVTCALLEYRLYRILGRKCGGGVASLWLLFQLTSAGMFISS 150

Query: 548 IALLPSSFAM 577  
ALLPSSF+M  
Sbjct: 151 AALLPSSFSM 160

FIGURE 12 (sheet 2)

*S. pombe*

Score = 104 bits (260), Expect = 1e-21  
 Identities = 58/157 (36%), Positives = 85/157 (54%)  
 Frame = +2

Query: 197 LISTFYGIISDCDEVFNWYWEPLNFMLRGFGKQTWEYSPEYAIRSWSYLVPLWIAGYPPLF 376  
 L S + +I DCDEV+NYWEPL+++L G+G QTWEYSPEYAIRSW Y+ + G+  
 Sbjct: 26 LTSASFRVIDDCDEVYNYWEPLHYLLYGYGLQTWEYSPEYAIRSWFYIALHAVPGFLARG 85

Query: 377 LDIPSXXXXXXXXRLLLVIFSLVAEVKLYHSLKKNVSSKISFWYLLFTTVAPGMSHSTIAL 556  
 L + R +L FS E L ++ +N + ++ V GM ++ +  
 Sbjct: 86 LGLSRLHVFYFIRGVLACFSAFCTENLILAVARNFNRAVALHLTSVLFVNSGMWSASTSF 145

Query: 557 LPSSFAMVCHTFAIRYVIDYLQPLTMLRTIRETAAIS 667  
 LPSSFAM T A+ L P+ RT++ + I+  
 Sbjct: 146 LPSSFAMNMVTLALS---AQLSPSTKRTVKVVSFIT 179

*M. musculus*

Score = 99.4 bits (246), Expect = 4e-20  
 Identities = 57/143 (39%), Positives = 76/143 (53%), Gaps = 1/143 (0%)  
 Frame = +2

Query: 152 SPTSCMYWPILS\*DLISTFYGIISDCDEVFNWYWEPLNFMLRGFGKQTWEYSPEYAIRSW 331  
 +P S + +LS L + ISDCDE FNYWEP ++++ G G QTWEYSP YAIRS+  
 Sbjct: 55 APEGSTAFKCLLSARLCAALLSNISDCDETFNYWEPHYLIYKGKFQTWEYSPVYAIRSY 114

Query: 332 SY-LVPLWIAGYPPLFLDIPSXXXXXXXXRLLLVIFSLVAEVKLYHSLKKNVSSKISFWYL 508  
 +Y L+ W A + L R LL S V E+ Y ++ K +S L  
 Sbjct: 115 AYLLHAWPAAFHARILQTNKILVFYFLRCLLAFVSCVCELYFYKAVCKKFGHLHVSRRML 174

Query: 509 LFTTVAPGMSHSTIALLPSSFAM 577  
 F ++ GM S+ A LPSSF M  
 Sbjct: 175 AFLVLSTGMFCSSSAFLPSSFCM 197

*H. sapiens*

Score = 99.4 bits (246), Expect = 4e-20  
 Identities = 56/143 (39%), Positives = 76/143 (53%), Gaps = 1/143 (0%)  
 Frame = +2

Query: 152 SPTSCMYWPILS\*DLISTFYGIISDCDEVFNWYWEPLNFMLRGFGKQTWEYSPEYAIRSW 331  
 +P S + +LS L + ISDCDE FNYWEP ++++ G G QTWEYSP YAIRS+  
 Sbjct: 55 APEGSTAFKCLLSARLCAALLSNISDCDETFNYWEPHYLIYGEGFQTWEYSPAYAIRSY 114

Query: 332 SY-LVPLWIAGYPPLFLDIPSXXXXXXXXRLLLVIFSLVAEVKLYHSLKKNVSSKISFWYL 508  
 +Y L+ W A + L R LL S + E+ Y ++ K +S L  
 Sbjct: 115 AYLLHAWPAAFHARILQTNKILVFYFLRCLLAFVSCICELYFYKAVCKKFGHLHVSRRML 174

Query: 509 LFTTVAPGMSHSTIALLPSSFAM 577  
 F ++ GM S+ A LPSSF M  
 Sbjct: 175 AFLVLSTGMFCSSSAFLPSSFCM 197

FIGURE 13

*S. cerevisiae* ALG12

ATGCGTTGGTCTGTCCTTGATACAGTGCTATTGACCGTGATTTTCCTTTCATCTAAT  
 CCAAGCTCCATTACCAAGGTGGAAGAGAGTTTTAATATTCAAGCCATTCATGAT  
 ATTTTAACCTACAGCGTATTTGATATCTCCCAATATGACCACTTGAAATTTCTGG  
 AGTAGTCCCTAGAACATTCGTTGGTGCTGTGATTATTGCAATGCTTTTCGAGACCTT  
 ATCTTTACTTGAGTTCTTTGATCCAACTTCCAGGCCTACGTCTATAGATGTTCAA  
 TTGGTCGTTAGGGGGATTGTTGGCCTACCAATGGGCTTTCTTTTATCTATTTAAA  
 GAATTGTTTGCAAGATATGTTTGATGAAATCACTGAAAAGAAAAAGGAAGAAAA  
 TGAAGACAAGGATATATACATTTACGATAGCGCTGGTACATGGTTTCTTTTATTTT  
 TAATTGGCAGTTTCCACCTCATGTTCTACAGCACTAGGACTCTGCCTAATTTTGTC  
 ATGACTCTGCCTCTAACCAACGTCGCATTGGGGTGGGTTTTATTGGGTCGTTATAA  
 TGCAGCTATATTCCTATCTGCGCTCGTGGCAATTGTATTTAGACTGGAAGTGTCAG  
 CTCTCAGTGCTGGTATTGCTCTATTTAGCGTCATCTTCAAGAAGATTTCTTTATTC  
 GATGCTATCAAATTCGGTATCTTTGGCTTGGGACTTGGTTCGCCATCAGTATCAC  
 CGTTGATTATATTTCTGGCAAGAATGGTGTCTACCTGAGGTAGATGGTTTCTTGT  
 TCAACGTGGTTGCGGGTTACGCTTCCAAGTGGGGTGTGGAGCCAGTTACTGCTTA  
 TTTCACGCATTACTTGAGAATGATGTTTATGCCACCAACTGTTTTACTATTGAATT  
 ACTTCGGCTATAAATTAGCACCTGCAAAATTAAAAATTGTCTCACTAGCATCTCTT  
 TTCCACATTATCGTCTTATCCTTTCAACCTCACAAGAATGGAGATTCATCATCTA  
 CGCTGTTCCATCTATCATGTTGCTAGGTGCCACAGGAGCAGCACATCTATGGGAG  
 AATATGAAAGTAAAAAAGATTACCAATGTTTTATGTTTGGCTATATTGCCCTTATC  
 TATAATGACCTCCTTTTTTCATTTCAATGGCGTTCTTGTATATATCAAGAATGAATT  
 ATCCAGGCGGCGAGGCTTTAACTTCTTTTAATGACATGATTGTGGAAAAAATAT  
 TACAAACGCTACAGTTCATATCAGCATACCTCCTTGCATGACAGGTGTCATTTTAT  
 TTGGTGAATTGAACTACGGTGTGTACGGCATCAATTACGATAAGACTGAAAATAC  
 GACTTTACTGCAGGAAATGTGGCCCTCCTTTGATTTCTTGATCACCCACGAGCCA  
 ACCGCCTCTCAATTGCCATTCGAGAATAAGACTACCAACCATTGGGAGCTAGTTA  
 ACACAACAAAGATGTTTACTGGATTTGACCCAACCTACATTAAGAACTTTGTTTT  
 CCAAGAGAGAGTGAATGTTTTGTCTCTACTCAAACAGATCATTTTCGACAAGACC  
 CCTACCGTTTTTTTTGAAAGAATTGACGGCCAATTCGATTGTTAAAAGCGATGTCTT  
 CTTACCTATAAGAGAATCAAACAAGATGAAAAAACTGATTGA

*S. cerevisiae* Alg12p

MRWSVLDTVLLTVISFHLIQAPFTKVEESFNIQAIHDILTYSVFDISQYDHLKFPGVVP  
 RTFVGAVIAMLSPYLYLSSLIQTSRPTSIDVQLVVRGIVGLTNGLSFIYLNCLQDM  
 FDEITEKKKEENEDKDIYIYDSAGTWFLFLIGSFHLMFYSTRTLPNFVMTLPLTNVAL  
 GWVLLGRYNAAIFLSALVAIVFRLEVSALSAGIALFSVIFKKISLFDKIFGIFGLGLGS  
 AISITVDSYFWQEWCLPEVDGFLFNVVAGYASKWGVPEPVTAYFTHYLRMMFMPPTV  
 LLLNYFGYKLAPAKLKIVSLASLFHIIVLSFQPHKEWRFIYAVPSIMLLGATGAHLW  
 ENMKVKKITNVLCAILPLSIMTSFFISMAFLYISRMNYPGGEALTSFNDMIVEKNITN  
 ATVHISIPPCMTGVTLFGELNYGVYGINYDKTENTLLQEMWPSFDFLITHEPTASQLP  
 FENKTTNHVELVNTTKMFTGFDPTYIKNFVFQERVNVLSLLKQIIFDKTPTVFLKELT  
 ANSIVKSDVFFTYKRIKQDEKTD

FIGURE 14

*P. pastoris* ALG12

TCGGTCGAGAATGATAACTGAAGAACTCAAAATCTCTCACACTTTTCATCGT  
TACTGTACTGGCAATCATTGCATTTTCAGCCTCATAAAGAATGGAGATTTAT  
AGTTTACATTGTTCCACCACTTGTCATCACCATATCTACAGTACTTGCACA  
ACTACCCAGGAGATTCACAATCGTCAAAGTTGCTGTTTTTCTCCTAAGTTT  
CGGCTCTTTGCTCATATCCCTGTCGTTTCTTTTCATCTCATCGTATAACTAC  
CCTGGGGGGTGAAGCTTTACAGCATTGGAACGAGAACTCCTTCTACTGGA  
CCAAAGTTCCCTACCTGTTGATATTAAGGTTTCATATGGATGTCCCTGCATG  
CATGACTGGGGTGACTTTATTTGGTTACTTGGATAACTCAAAATTGAACAA  
TTTAAGAATTGTCTATGATAAAACAGAAGACGAGTCGCTGGACACAATCT  
GGGATTCTTTCAATTATGTCATCTCCGAAATTGACTTGGATTCTTCGACTG  
CTCCCAAATGGGAGGGGGGATTGGCTGAAGATTGATGTTGTCCAAGGCTAC  
AACGGCATCAATAAACAATCTATCAAAAATACAATTTTCAATTATGGAAT  
ACTTAAACGGATGATAAGAGACGCAACCAAACCTTGATGTTGGATTTATTC  
GTACGGTCTTTTCGATCCTTCATAAAATTTGATGATAAATTATTCATTTATG  
AGAGGAGCAGTCAAACCTGAAAATATATACCTCATTTGTTCAATTTGGTGT  
AAAGAGTGTGGCGGATAGACTTCTTGTAATCAGGAAAGCTACAATTCCA  
ATTGCTGCAAAAAATACCAATGCCCATAA

*P. pastoris* Alg12p

RMITEELKISHTFIVTVLAIIAFQPHKEWRFIVYIVPPLVITISTVLAQLPRRFTIV  
KVAVFLLSFGSLLISLSFLFISSYNYPGGEALQHLNEKLLLLDQSSLPVDIKVH  
MDVPACMTGVTLFGYLDNSKLNLRIVYDKTEDESLDTIWDSFNYSVISEIDL  
SSTAPKWECDWLKIDVVQGYNGINKQSIKNTIFNYGILKRMIRDATKLDVGF  
RTVFRSFIKFDDKLFYIERSSQ

FIGURE 15 (sheet 1)

*P. pastoris* ALG12 BLAST

Sequences producing significant alignments:

	Score	E
	(bits)	Value

gi 1302525 emb CAA96310.1	ORF YNR030w [Saccharomyces cerev...]	102	5e-21
gi 19112221 ref NP_595429.1	putative involvement in cell w...	56	5e-07
gi 15864569 emb CAC83681.1	putative dolichyl-p-man: Man7G1...	53	4e-06
gi 13129114 ref NP_077010.1	dolichyl-p-mannose:Man7GlcNAc2...	53	4e-06
gi 22266724 gb AAM94900.1 AF311904.1	membrane protein SB87 ...	53	4e-06
gi 18478284 emb CAD22101.1	putative mannosyltransferase [M...	52	8e-06

## Alignments

*S. cerevisiae*

Score = 102 bits (255), Expect = 5e-21

Identities = 74/258 (28%), Positives = 121/258 (46%), Gaps = 19/258 (7%)

Query: 8 RMITEELKISHTFIVTVLAIIAFQPHKEWRFIVYIVPPLVITISTVLAQLPRRFTIVKVA 187  
 ++ +LKI + + +++FQPHKEWRFI+Y VP +++ +T A L + K+

Sbjct: 302 KLAPAKLKIVSLASLFHIIIVLSFQPHKEWRFIIYAVPSIMLLGATGAHLWENMKVKKIT 361

Query: 188 -----VXXXXXXXXXXXXXXXXXXNYPGGEALQHLNEKLLLLDQSSLPVDIKVHMD 346  
 + NYPGGEAL N+ ++ + VH+

Sbjct: 362 NVLCLAILPLSIMTSFFISMAFLYISRMNYPGGEALTSFNDMIV----EKNITNATVHIS 417

Query: 347 VPACMTGVTLFGYLDNSKLNLRIVYDKTEDES-LDTIWDSFNYVI-----SEIDLSS 505  
 +P CMTGVTLEFG L+ I YDKTE+ + L +W SF+++I S++ ++

Sbjct: 418 IPPCMTGVTLEFGELNYGVY---IN YDKTENTTLLQEMWPSFDLITHEPTASQLPFENK 474

Query: 506 TAPKWECDWLKIDVVQGYNGINKQSIKNTIFN-----YGILKRMIRDATKLDVGFIRTVF 670  
 T WE ++ + + G + IKN +F +LK++I D K F++ +

Sbjct: 475 TTNHWE----LVNTTKMFTGFDPTYIKNFVFQERVNVLSSLKQIIFD--KTPTVFLKELT 528

Query: 671 RSFIKFDKLFYIERSSQ 724  
 + I D F Y+R Q

Sbjct: 529 ANSIVKSDVFFTYKRIKQ 546

*S. pombe*

Score = 56.2 bits (134), Expect = 5e-07

Identities = 46/152 (30%), Positives = 62/152 (40%), Gaps = 11/152 (7%)

Query: 65 IIAFQPHKEWRFIVYIVPPLVITISTVLAQL-----PRRFTIVKVAVXXXXXXXXXX 220  
 + +F HKEWRFI+Y + P S + A L + F I+++

Sbjct: 295 VYSFLGHKEWRFIIYSI-PWFNAASAIGASLCFNASKFGKKIFEILRLMFFSGIIFGFIG 353

Query: 221 XXXXXXXXXXXNYPGGEALQHLNEKLLLLDQSSLPVDIKVHMDVPACMTGVTLEFGYLDNSK 400  
 Y YPGG AL L E + VHMDV CMTG+T F L +

Sbjct: 354 SSFLLYVFQYAYPGGLALTRLYE-----IENHPQVSVHMDVYPCMTGITRFSQLPS-- 404

FIGURE 15 (sheet 2)

Query: 401 LNNLRIVYDKTEDESL---DTIWDSFNYVISE 487  
                   YDKTED +                   F+Y+I+E  
 Sbjct: 405 -----WYYDKTEDPKMLSNSLFISQFDYLITE 431

Homo sapiens

Score = 53.1 bits (126), Expect = 4e-06  
 Identities = 41/149 (27%), Positives = 68/149 (45%), Gaps = 6/149 (4%)

Query: 59 LAIIAFQPHKEWRFIVYIVPPLVITISTVLAQLPRR-----FTIVKVAVXXXXXXXXXX 220  
           +A+ + PHKE RFI+Y P L IT + + L + + V

Sbjct: 299 MALYSLLPHKELRFIIYAFPMLNITAARGCSYLLNNYKKSPLYKAGSLLVIGHLVVNAAY 358

Query: 221 XXXXXXXXXYNYPGGEALQHLNEKLLLLDQSSLFVDIKVHMDVPACMTGVTLFGYLDNSK 400  
           +NYPGG A+Q L++ L+ Q+ D+ +H+DV A TGV+ F ++++

Sbjct: 359 SATALYVSHFNYPGGVAMQRLHQ--LVPPQT---DVLLHIDVAAAQTGVSRLQVNSAW 412

Query: 401 LNNLRIVYDKTEDESLDTIWDSFNYVISE 487  
                   YDK ED T ++ +++ E

Sbjct: 413 R-----YDKREDVQPGTGMLAYTHILME 435

# Applied Biosystems Voyager System 6235

Voyager Spec #1[BP = 1463.3, 2852]

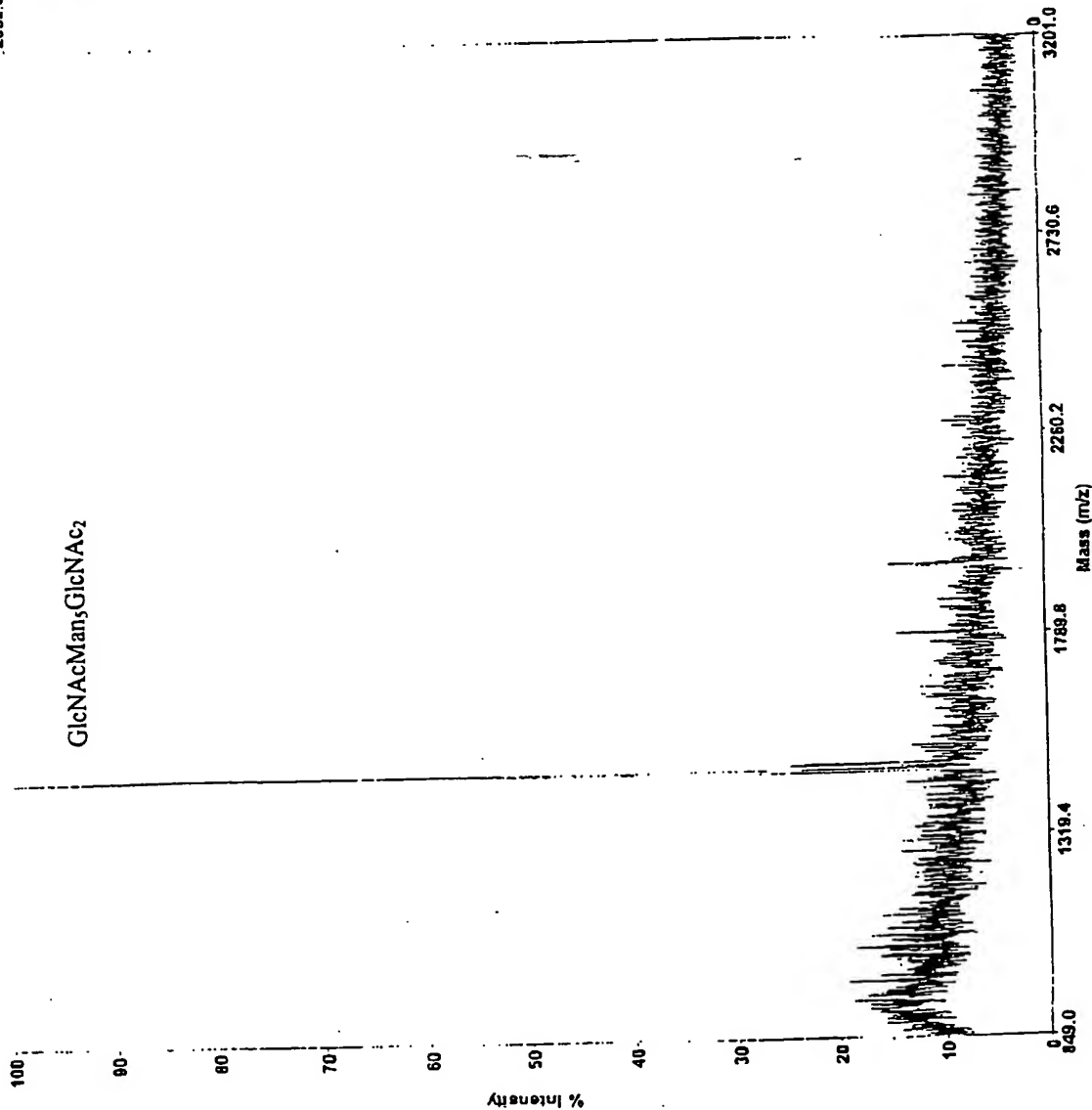


FIGURE 16

Mode of operation: Linear  
 Extraction mode: Delayed  
 Polarity: Positive  
 Manual  
 .2852.0 Acquisition control:  
 Accelerating voltage: 20000 V  
 Grid voltage: 93%  
 Guide wire O: 0.1%  
 Extraction delay time: 125 nsec  
 Acquisition mass range: 850 -- 3200 Da  
 Number of laser shots: 200/spectrum  
 Laser intensity: 2786  
 Laser Rep Rate: 20.0 Hz  
 Calibration type: Default  
 Calibration matrix: a-Cyano-4-hydroxydynamic ac  
 Low mass gate: 800 Da  
 Digitizer start time: 19.955  
 Bin size: 0.5 nsec  
 Number of data points: 37310  
 Vertical scale: 500 mV  
 Vertical offset: 0%  
 Input bandwidth: 500 MHz  
 Sample well: 22  
 Plate ID: 100 WELL PLATE  
 Serial number: 6235  
 Instrument name: Voyager-DE PRO  
 Plate type filename: C:\VOYAGER\100 well plate.pl  
 Lab name: PE Biosystems  
 Absolute x-position: 6212.96  
 Absolute y-position: 35933.8  
 Relative x-position: -454.524  
 Relative y-position: -1213.7  
 Shots in spectrum: 200  
 Source pressure: 6.504e-007  
 Mirror pressure: 8.818e-008  
 TC2 pressure: 0.01188  
 TIS gate width: 10  
 TIS flight length: 689

Printed: 10:47, December 18, 200

Acquired: 11:42:00, November 08, 2002

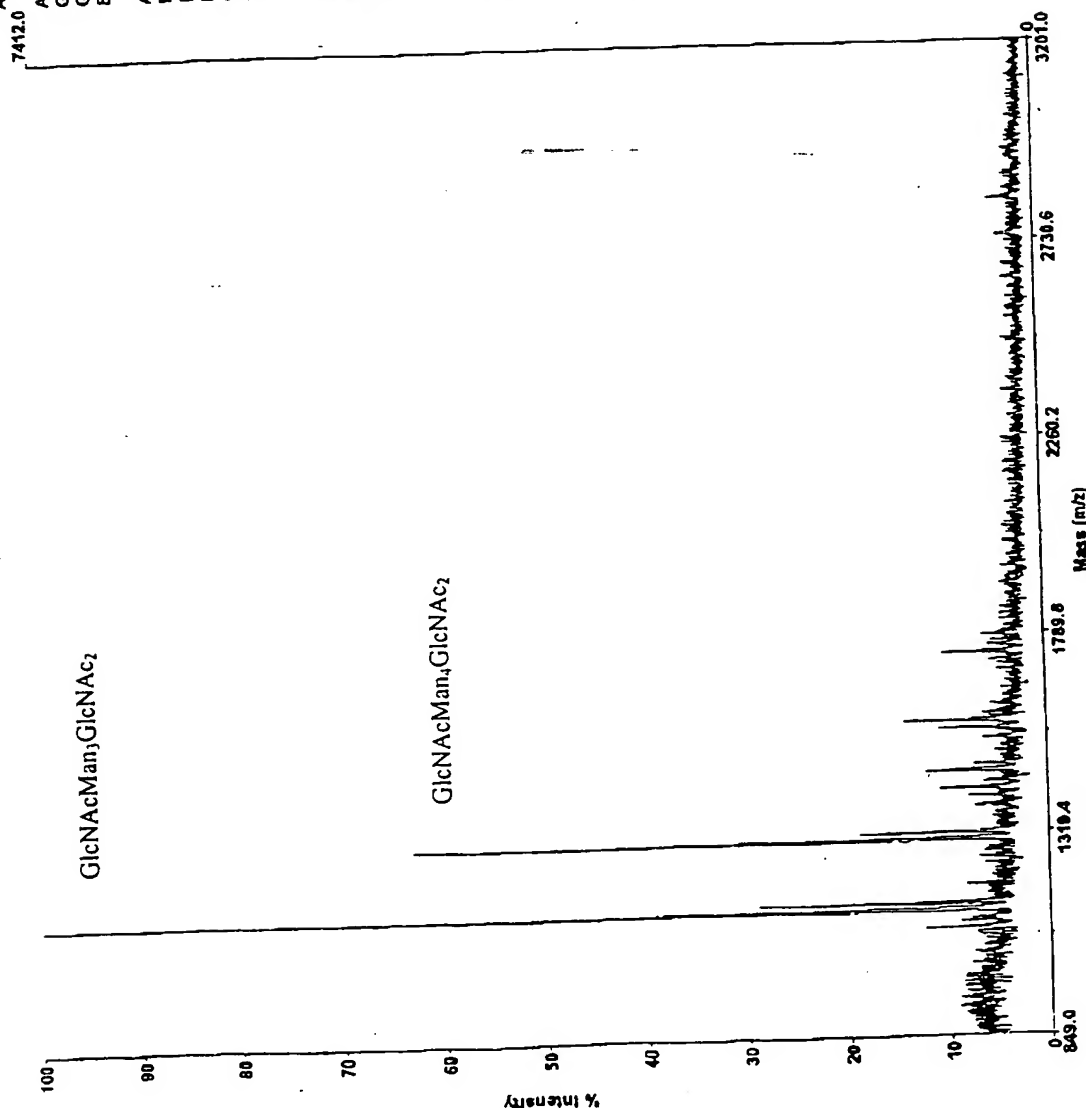




# Applied Biosystems voyager system

Voyager Spec #1[BP = 1137.8, 7412]

FIGURE 18



Mode of operation: Linear  
 Extraction mode: Delayed  
 Polarity: Positive  
 Acquisition control: Manual  
 Accelerating voltage: 20000 V  
 Grid voltage: 93%  
 Guide wire 0: 0.1%  
 Extraction delay time: 125 nsec  
 Acquisition mass range: 850 - 3200 Da  
 Number of laser shots: 200/spectrum  
 Laser intensity: 2985  
 Laser Rep Rate: 20.0 Hz  
 Calibration type: Default  
 Calibration matrix: n-Cyano-4-hydroxymethyl a  
 Low mass gate: 800 Da  
 Digitizer start time: 18.855  
 Bin size: 0.5 nsec  
 Number of data points: 37310  
 Vertical scale: 500 mV  
 Vertical offset: 0%  
 Input bandwidth: 500 MHz  
 Sample well: 03  
 Plate ID: 100 WELL PLATE  
 Serial number: 6235  
 Instrument name: Voyager-DE PRO  
 Plate type filename: C:\VOYAGER\100 well plate.  
 Lab name: PE Biosystems  
 Absolute x-position: 12910.9  
 Absolute y-position: 46669.9  
 Relative x-position: 1163.37  
 Relative y-position: -637.62  
 Shots in spectrum: 200  
 Source pressure: 1.781e-008  
 Mirror pressure: 1.525e-007  
 TC2 pressure: 0.01459  
 TIS gate width: 90  
 TIS flight length: 889

Printed: 11:47, December 17, .

Acquired: 10:16:00, October 13, 2002  
 D:\Data\HujianData for burn\Other samples\OCT 2002\10-13-02\Rob-3\_0002.dai

# Applied Biosystems Voyager System 6235

Voyager Spec #1[BP = 1139.5, 4716]

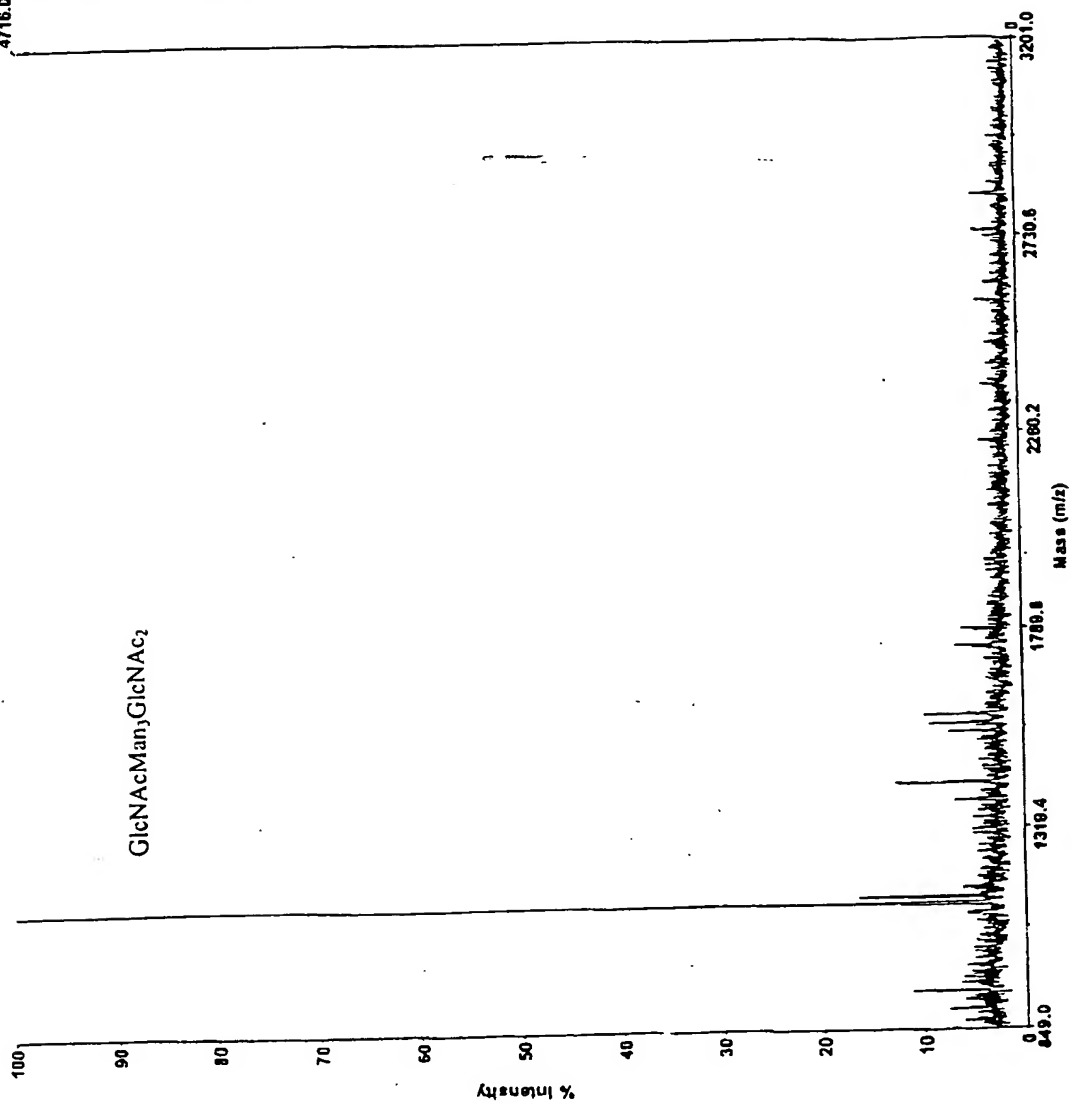


FIGURE 19

Mode of operation: Linear  
Extraction mode: Delayed  
Polarity: Positive  
Acquisition control: Manual  
Accelerating voltage: 20000 V  
Grid voltage: 93%  
Guide wire 0: 0.1%  
Extraction delay time: 125 nsec  
Acquisition mass range: 850 - 3200 Da  
Number of laser shots: 200/spectrum  
Laser intensity: 2766  
Laser Rep Rate: 20.0 Hz  
Calibration type: Default  
Calibration matrix: a-Cyano-4-hydroxynaphthamic  
Low mass gate: 800 Da  
Digitizer start time: 19.955  
Bin size: 0.5 nsec  
Number of data points: 37310  
Vertical scale: 500 mV  
Vertical offset: 0%  
Input bandwidth: 500 MHz  
Sample well: 24  
Plate ID: 100 WELL PLATE  
Serial number: 6235  
Instrument name: Voyager-DE PRO  
Plate type filename: C:\VOYAGER\100 well plate.j  
Lab name: PE Biosystems  
Absolute x-position: 18177.2  
Absolute y-position: 37530.3  
Relative x-position: 1349.67  
Relative y-position: 382.81  
Shots in spectrum: 200  
Source pressure: 1.399e-006  
Mirror pressure: 1.235e-007  
TC2 pressure: 0.01248  
TIS gate width: 10  
TIS flight length: 689

Printed: 12:15, December 17, 2001

Acquired: 15:39:00, October 15, 2002

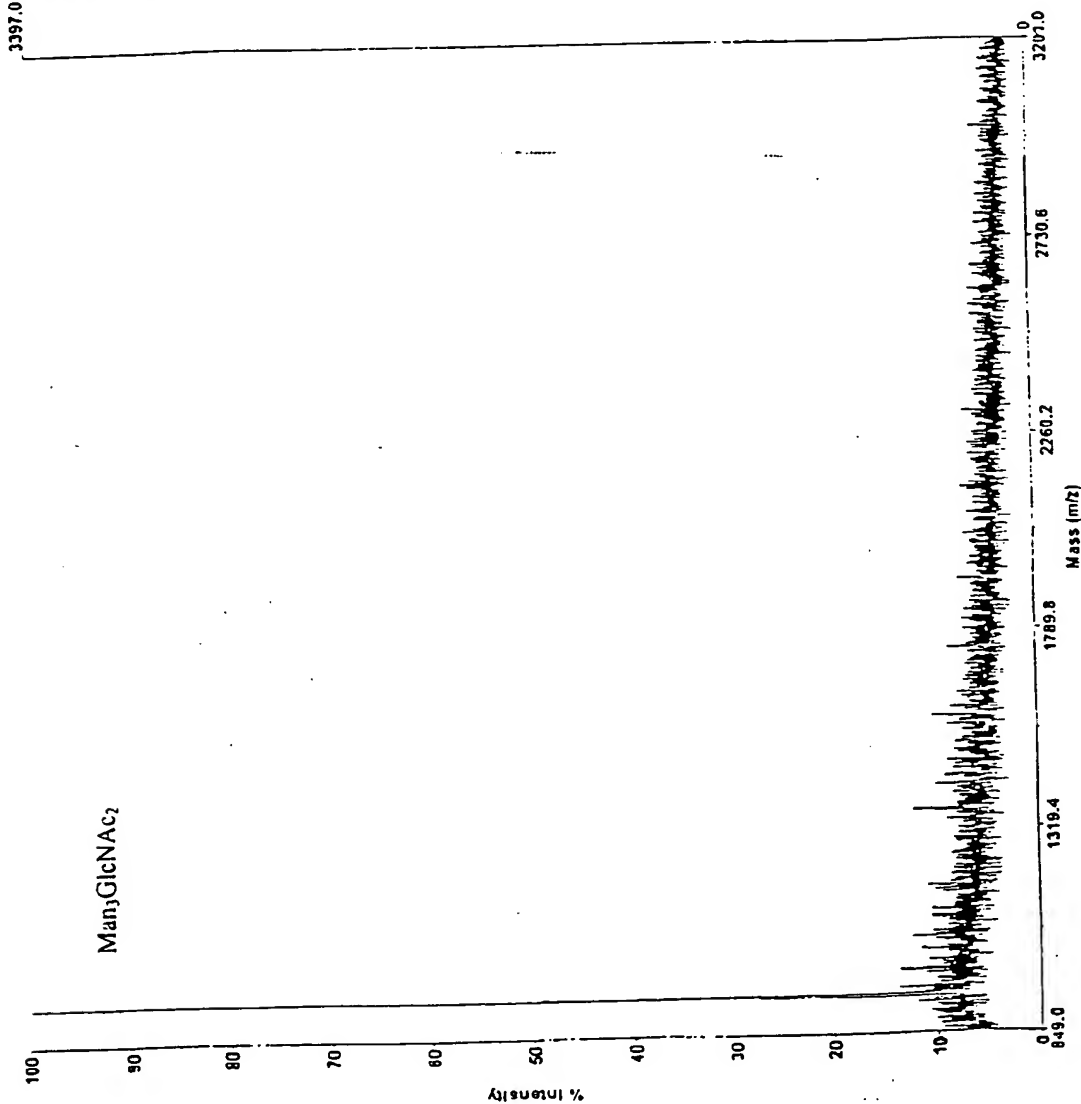
D:\Data\HuanData for burn\Other samples\OCT 2002\10-15-02\6D 10-10-02 3 1.2\digest\_0004.dai

# Applied Biosystems Voyager System 6235

Voyager Spec #1[BP = 935.7, 3397]

FIGURE 20

Mode of operation: Linear  
Extraction mode: Delayed  
Polarity: Positive  
Acquisition control: Manual  
Accelerating voltage: 20000 V  
Grid voltage: 93%  
Guide wire U: 0.1%  
Extraction delay time: 125 nsec  
Acquisition mass range: 850 - 3200 Da  
Number of laser shots: 200/spectrum  
Laser intensity: 2600  
Laser Rep Rate: 20.0 Hz  
Calibration type: Default  
Calibration matrix: a-Cyano-4-hydroxymethyl  
Low mass gate: 800 Da  
Digitizer start time: 19.955  
Pin size: 0.5 nsec  
Number of data points: 37310  
Vertical scale: 500 mv  
Vertical offset: 0%  
Input bandwidth: 500 MHz  
Sample well: 22  
Plate ID: 100 WELL PLATE  
Serial number: 6235  
Instrument name: Voyager-DE PRO  
Plate type filename: C:\VOYAGER\100 well plate.t  
Lab name: PE Biosystems  
Absolute x-position: 5518.88  
Absolute y-position: 37692.8  
Relative x-position: -1148.62  
Relative y-position: 545.303  
Shots in spectrum: 200  
Source pressure: 6.934e-007  
Minor pressure: 8.466e-008  
TCZ pressure: 0.01269  
TIS gate width: 10  
TIS flight length: 689



Printed: 12:05, December 17, 2002

Acquired: 14:31:00, November 27, 2002

D:\Data\Hull\anData for burn\Other samples\WOW 20V211-26-02\TH 11-20-02 RDP-27 hexo +1,2 hexosidase\_0001.dat

# Applied Biosystems Voyager System 6235

Voyager Spec #1[BP = 1356.8, 5565]

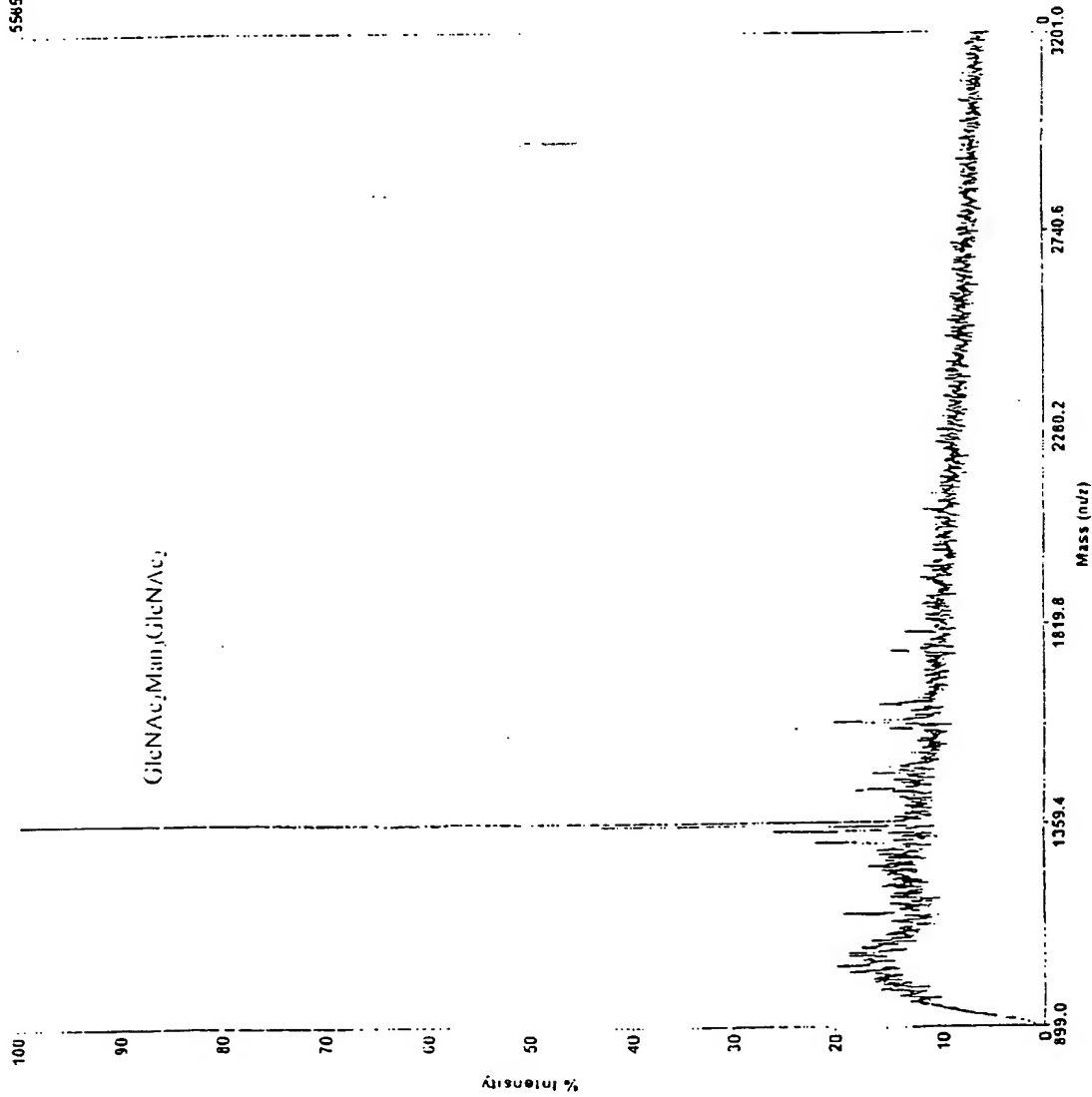


FIGURE 21

5565.2 Acquisition control: Linear  
 Mode of operation: Delayed  
 Extraction mode: Positive  
 Polarity: Automatic  
 Accelerating voltage: 20000 V  
 Grid voltage: 93%  
 Guide wire Q: 0.1%  
 Extraction delay time: 125 msec  
 Acquisition mass range: 900 - 3200 Da  
 Number of laser shots: 100/spectrum  
 Laser intensity: 2882  
 Laser Rep Rate: 20.0 Hz  
 Calibration type: Default  
 Calibration matrix: 3-Cyano-4-hydroxycinnamic acid  
 Low mass gate: 875 Da  
 Digital start time: 20.5305  
 On size: 0.5 msec  
 Number of data points: 36159  
 Vertical scale: 500 mV  
 Vertical offset: 0%  
 Input transducer: SUT-Me 12  
 Laser control: Manual  
 Sample positioning: Automated  
 Etchdown Pattern: Edge Etched  
 Auto storage mode: Accumulate all passing  
 Min intensity: 224  
 Max intensity: 0  
 Resolution: 0  
 Signal-to-noise: 3  
 Sample well: 91  
 Plate ID: 100 WELL PLATE  
 Serial number: 6235  
 Instrument name: Voyager-DE PRO  
 Plate type filename: C:\VOYAGER\100 well plate.p  
 Lab name: PE Biosystems  
 Absolute x-position: 1190.1  
 Absolute y-position: 2397.25  
 Relative x-position: -397.403  
 Relative y-position: 809.751  
 Shots in spectrum: 500  
 Source pressure: 9.936e-007  
 Mirror pressure: 9.246e-008  
 TCZ pressure: 0.0122  
 TIS gate width: 10  
 TIS flight length: 609

Printed: 10/59, December 14, 2001

Acquired: 12:57:00, October 28, 2002

Sample Description: .

Comments:

D:\Data\Huijuan\Data for burn\Screen data\October 2002\UN Media digest 10-23-02 WFB-JUN LA 10-32 IV 10-24-02 91\_0001.dai

# Applied Biosystems Voyager System 6235

Voyager Spec #1 [BP = 934.5, 7357]

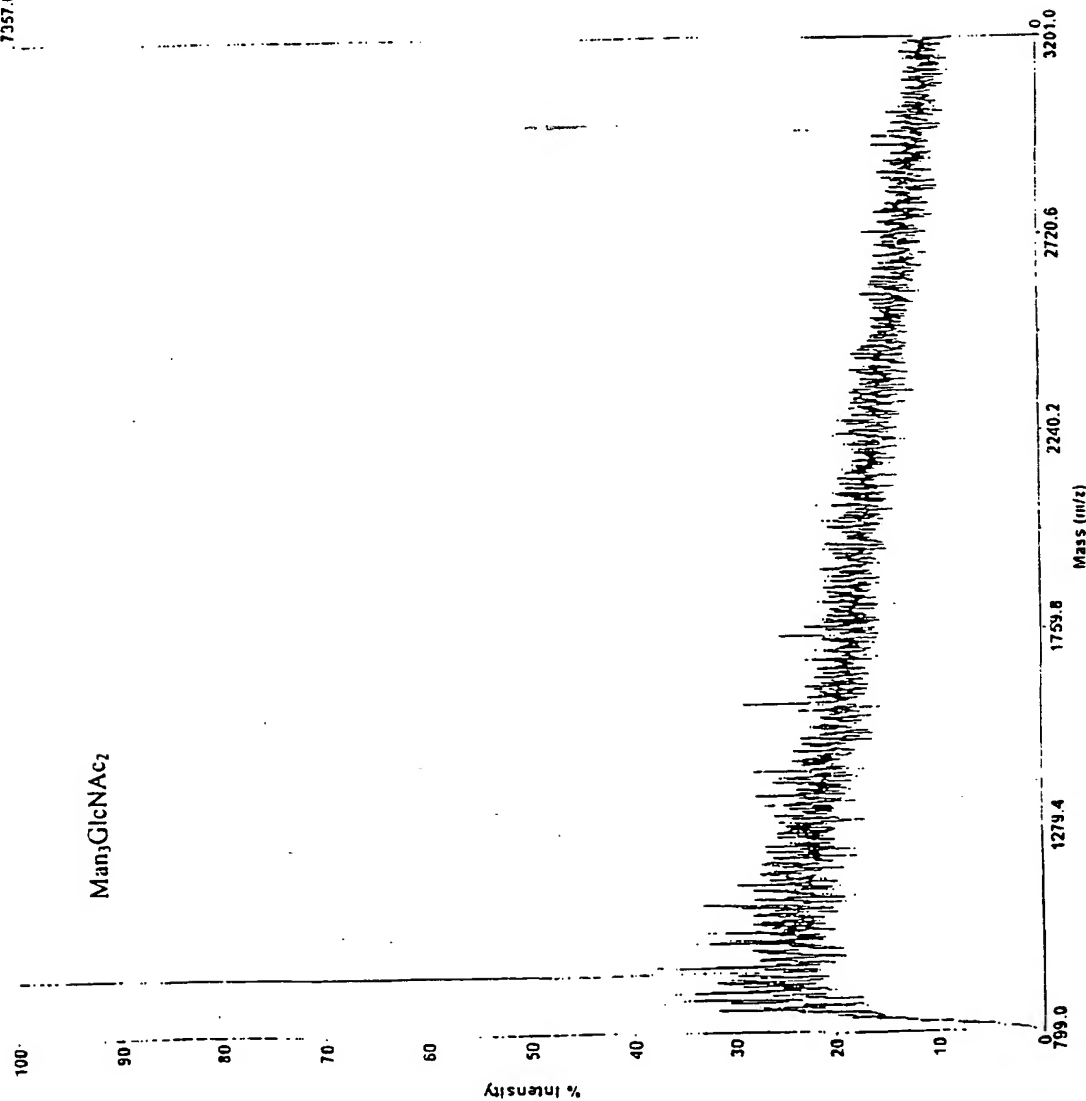


FIGURE 22

Mode of operation: Linear  
Extraction mode: Delayed  
Polarity: Positive  
Acquisition control: Manual  
7357.0  
Accelerating voltage: 19000 V  
Grid voltage: 94%  
Guide wire D: 0.15%  
Extraction delay time: 175 nsec  
Acquisition mass range: 800 -- 3200 Da  
Number of laser shots: 150/spectrum  
Laser intensity: 3052  
Laser Rep Rate: 20.0 Hz  
Calibration type: Default  
Calibration matrix: α-Cyano-4-hydroxycinnamic acid  
Low mass gate: 800 Da  
Digitizer start time: 19.8845  
Bin size: 0.5 msec  
Number of data points: 39555  
Vertical scale: 500 mV  
Vertical offset: 0%  
Input bandwidth: 500 MHz  
Sample well: 91  
Plate ID: 100 WELL PLATE  
Serial number: 0235  
Instrument name: Voyager-DE PRO  
Plate type identifier: C:\VOYAGER\100 well plate.p  
Lab name: PE Biosystems  
Absolute x-position: 1843.77  
Absolute y-position: 306.377  
Relative x-position: 256.268  
Relative y-position: -1281.12  
Shots in spectrum: 150  
Source pressure: 8.671e-007  
Mirror pressure: 8.165e-008  
TC2 pressure: 0.01199  
TIS gate width: 10  
TIS light length: 689

Printed: 10:59, December 18, 2000

Acquired: 08:30:00, October 30, 2002

D:\Data\Hulian\Data for burn\Screen data\October 2002\PB-JN LA 30-32 10-24-02 IV\PB-JN LA 30-32 10-24-02 911lexo digest\_0007.dat

# Applied Biosystems Voyager System 6235

Voyager Spec #1[BP = 1666.9, 3309]

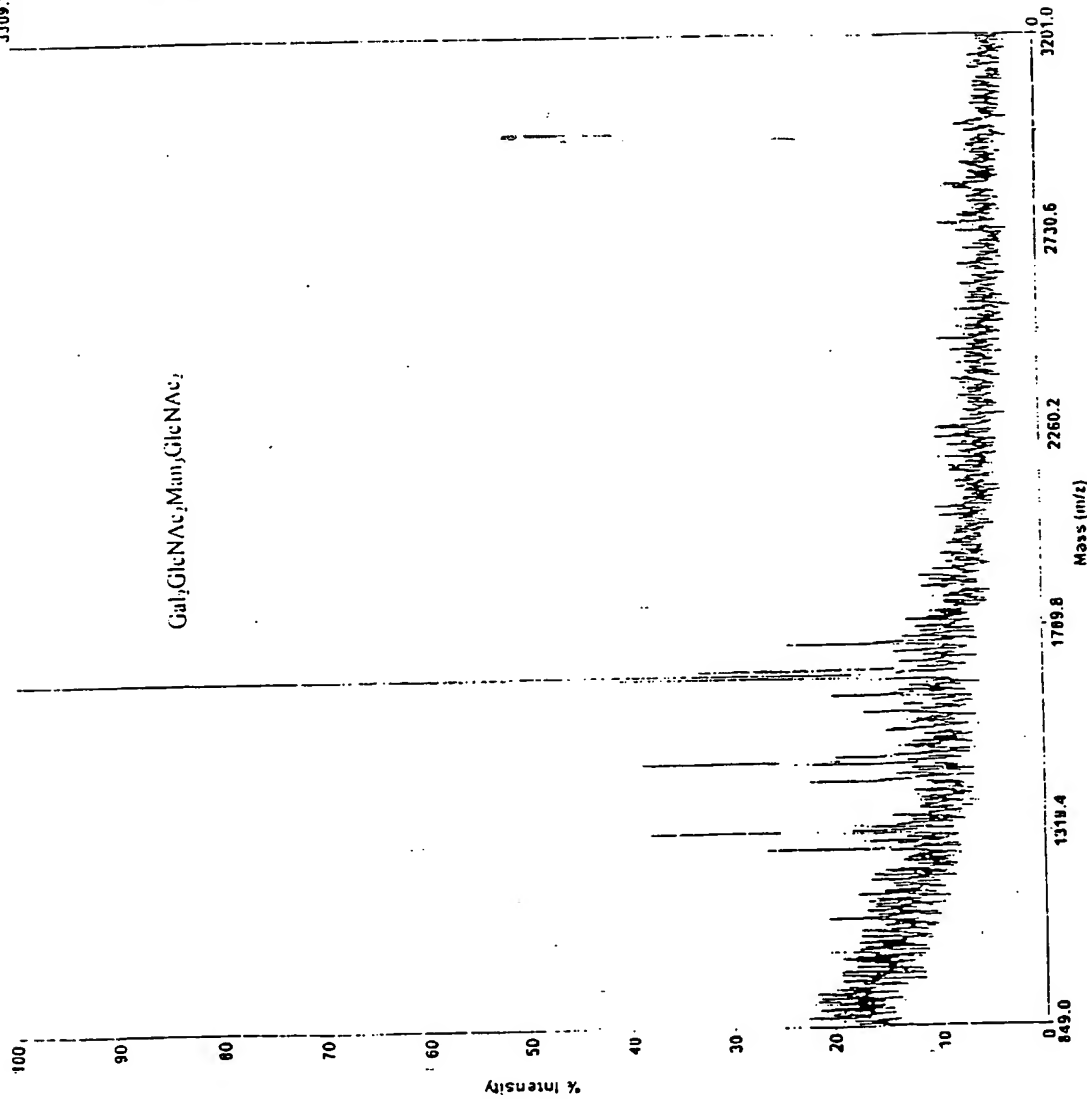


FIGURE 23

Mode of operation: Linear  
Extraction mode: Delayed  
Polarity: Positive  
Acquisition control: Manual  
3309.1 Acquisition control: Manual  
Accelerating voltage: 20000 V  
Grid voltage: 50%  
Guide wire U: 0.1%  
Extraction delay time: 125 msec  
Acquisition mass range: 850 - 3200 Da  
Number of laser shots: 2000/spectrum  
Laser intensity: 2000  
Laser Rep Rate: 20.0 Hz  
Calibration type: Default  
Calibration matrix: a-Cyano-4-hydroxycinnamic  
Low mass gate: 800 Da  
Digitizer start time: 19.955  
Ion size: 0.5 msec  
Number of data points: 37310  
Vertical scale: 500 mV  
Vertical offset: 0%  
Input bandwidth: 500 kHz  
Sample well: 77  
Plate ID: 100 WELL PLATE  
Serial number: 0235  
Instrument name: Voyager-UE PRO  
Plate type filename: C:\VOYAGER\100 well plate.p  
Lab name: PE Biosystems  
Absolute x position: 3.8113 1  
Absolute y position: 1.2244 9  
Relative x position: 945.594  
Relative y position: 513.403  
Shots in spectrum: 200  
Source pressure: 5.864e-007  
Mirror pressure: 7.263e-008  
TC2 pressure: 0.01159  
TIS gate width: 10  
TIS light length: 689

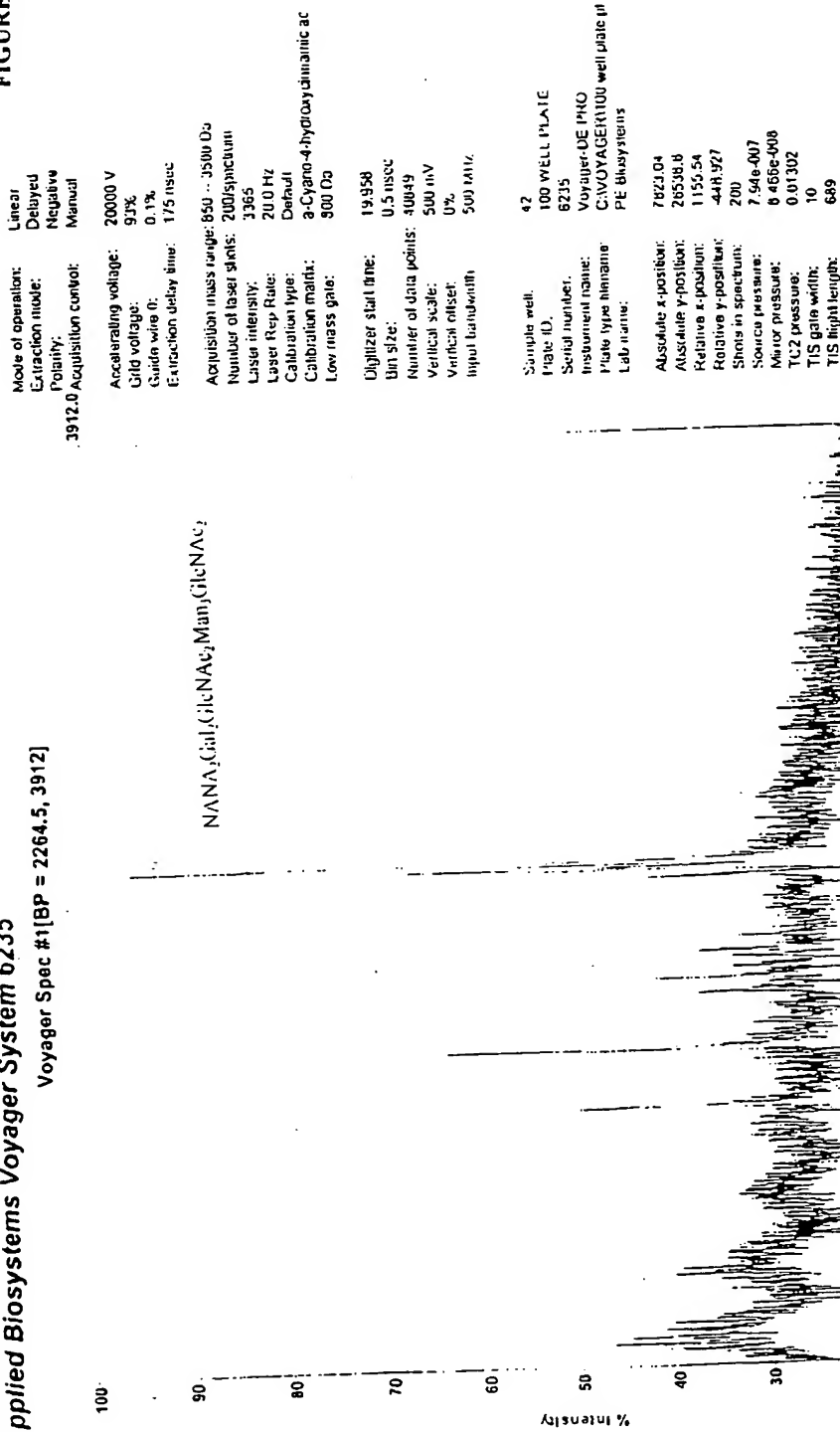
Printed: 11:02, December 19, 2002

Acquired: 11:05:00, December 07, 2002

C:\Instruments\Voyager\100\12-7-02\80th PAP6-S-Gal T\_0001.dat

FIGURE 24

Applied Biosystems Voyager System 6235  
Voyager Spec #1[BP = 2264.5, 3912]



Printed: 11/03, December 18, 2002

Acquired: 08:47:00, December 16, 2002  
D:\Data\Bios\BP8PC-2 c sialtrans\_0001.dat

FIGURE 25

*S. cerevisiae* ALG6

ATGGCCATTGGCAAAAGGTTACTGGTGAACAAACCAGCAGAAGAATCATT  
 TTATGCTTCTCCAATGTATGATTTTTTGTATCCGTTTAGGCCAGTGGGGAA  
 CCAATGGCTGCCAGAATATATTATCTTTGTATGTGCTGTAATACTGAGGTG  
 CACAATTGGACTTGGTCCATATTCTGGGAAAGGCAGTCCACCGCTGTACG  
 GCGATTTTGAGGCTCAGAGACATTGGATGGAAATTACGCAACATTTACCG  
 CTTTCTAAGTGGTACTGGTATGATTTGCAATACTGGGGATTGGACTATCCA  
 CCATTAACAGCATTTTCATTCGTACCTTCTGGGCCTAATTGGATCTTTTTTCA  
 ATCCATCTTGGTTTGCCTAGAAAAGTCACGTGGCTTTGAATCCCCCGATA  
 ATGGCCTGAAAACATATATGCGTTCTACTGTCATCATTAGCGACATATTGT  
 TTTACTTTTCTGCAGTAATATACTTTACTAAGTGGCTTGGTAGATATCGAA  
 ACCAGTCGCCCATAGGACAATCTATTGCGGCATCAGCGATTTTGTTC AAC  
 CTTTCATTAATGCTCATTGACCATGGGCCTTTCAATATAATTCAGTCATGC  
 TTGGCCTTACTGCTTATGCCATAAATACTTATTAGATGAGTATTATGCTA  
 TGGCGGCCGTTTGTGTTTGTCTATCCATTTGTTTTAAACAAATGGCATTGTA  
 TTATGCACCGATTTTTTTTTGCTTATCTATTAAGTCGATCATTGCTGTTCCCC  
 AAATTTAACATAGCTAGATTGACGGTTATTGCGTTTGCAACACTCGCAACT  
 TTTGCTATAATATTGCGCCATTATATTTCTTGGGAGGAGGATTAAAGAAT  
 ATTCACCAATGTATTCACAGGATATTCCTTTTGCCAGGGGCATCTTCGAA  
 GACAAGGTTGCTAACTTCTGGTGCGTTACGAACGTGTTTGTA AAAATACAA  
 GGAAAGATTCACTATACAACA ACTCCAGCTATATTCATTGATTGCCACCGT  
 GATTGGTTTCTTACCAGCCATGATAATGACATTACTTCATCCCAAAAAGCA  
 TCTTCTCCCATACGTGTTAATCGCATGTTTCGATGTCCTTTTTTCTTTTAGC  
 TTTCAAGTACATGAGAAA ACTATCCTCATCCCACTTTTGCCTATTACACTA  
 CTCTACTCCTCTACTGATTGGAATGTTCTATCTCTTGTAAGTTGGATAAAC  
 AATGTGGCTTTGTTTACGCTATGGCCTTTGTTGAAAAAGGACGGTCTTCAT  
 TTACAGTATGCCGTATCTTTCTTACTAAGCAATTGGCTGATTGGAAATTC  
 AGTTTTATTACACCAAGGTTCTTGCCAAAATCTTTAACTCCTGGCCCTTCT  
 ATCAGCAGCATCAATAGCGACTATAGAAGAAGAAGCTTACTGCCATATAA  
 TGTGGTTTGGAAAAGTTTTATCATAGGAACGTATATTGCTATGGGCTTTTA  
 TCATTTCTTAGATCAATTTGTAGCACCTCCATCGAAATATCCAGACTTGTG  
 GGTGTTGTTGAACTGTGCTGTTGGGTTCAATTGCTTTAGCATATTTTGGCTA  
 TGGTCTTATTACAAGATATTCATTCCGGTAGCAAATCCATGAAGGACTTG  
 TAG

*S. cerevisiae* ALG6p

MAIGKRLLVNKPAEESFYASPMYDFLYPFRPVGNQWLPEYIIFVCAVILRCTIG  
 LGPYSGKGSPLYGDFAQRHWMEITQHLPLSKWYWYDLQYWGLDYPPLTA  
 FHSYLLGLIGSFFNP SWFALEKSRGFESPDNGLKTYMRSTVIISDILFYFPAVIY  
 FTKWLGRYRNQSPIGQSIAASAILFQPSLMLIDHGHFQYNSVMLGLTAYAINN  
 LLDEYYAMAAVCFVLSICFKQMALYYAPIFFAYLLSRSLFPKFNIARLTVIAF  
 ATLATFAIIFAPLYFLGGGLKNIHQCIHRIFFARGIFEDKVANFWCVTNVFK  
 YKERFTIQQLQLYSLIATVIGFLPAMIMTLLHPKKHLLPYVLIACSMSFFLFSFQ  
 VHEKTILPILLPITLLYSSTDWNVLSLVSWINNVALFTLWPLLKKGDLHLQYA  
 VSFLLSNWLIGNFSFITPRFLPKSLTPGPSISSINS DYRRRSLLPYNVWKSFIIGT  
 YIAMGFYHFLDQFVAPPSKY PDLWVLLNCAVGFICFSIFWLWSYYKIFTSGSK  
 SMKDL



FIGURE 26

*P. pastoris* ALG6

ATGCCACATAAAAGAACGCCCTCTAGCAGTCTGCTGTATGCAAGAATTCC  
 AGGGATCTCTTTTGAAAACCTCTCCGGTGTGTTGATTTTTTTGTCTCCTTTTGA  
 CCCGCTCCTAATCAATGGGTAGCACGATACATCATCATCTTTGCAATT  
 CTCATCAGATTGGCAGTTGGGCTGGGCTCCTATTCCGGCTTCAACACCCCT  
 CCAATGTATGGGGATTTTGAAGCTCAGAGGCATTGGATGGAAATTACTCA  
 GCATTTATCCATAGAAAAATGGTACTTCTACGACTTGCAATATTGGGGGCT  
 TGACTIONCCTCCCTTGACAGCCTTTCATTACACTTCTTTGGCAAATTAGGC  
 AGCTTCATCAATCCAGCATGGTTTGCTTTAGACGTCTCCAGAGGGTTTGAA  
 TCAGTGGATCTAAAATCGTACATGAGGGCGACCGCAATTCTCAGTGAGCT  
 GTTATGTTTTATTCCAGCTGTCATTTGGTATTGTCGTTGGATGGGACTTAAC  
 TACTTCAATCAAAACGCCATTGAGCAAACATAATAGCGTCTGCTATTCTT  
 TTCAATCCATCTTTAATTATCATAGATCATGGCCACTTCCAGTACAACCTCA  
 GTTATGCTAGGTTTTGCTTTATTATCCATATTAAATCTGTTGTACGATAATT  
 TTGCATTAGCGGCTATTTTTTTCGTTCTTTCAATAAGCTTTAAGCAAATGGC  
 TCTCTATTATAGCCCCATCATGTTTTTTTACATGCTGAGTGTGAGTTGTTGG  
 CCTTTGAAAAACTTCAACTTGTTGAGATTGGCTACTATCAGTATTGCAGTA  
 CTCTTGACTTTTGCAACTCTATTACTGCCTTTTGTATTAGTAGATGGGATGT  
 CACAAATTGGCCAAATATTATTAGAGTTTTCCCGTTTTCAAGAGGCTTGT  
 TTGAGGATAAGGTGGCCAACTTTTGGTGTACAACGAATATACTGGTAAAG  
 TACAAACAGTTATTCACTGACAAAACCCTTACTAGGATATCGCTAGTAGC  
 AACTTTGATTGCAATTAGTCCGTCTTGCTTCATCATTTTTTACTCACCCAAAG  
 AAGGTTTTACTACCGTGGGCTTTTGCTGCTTGCTCTTGGGCGTTCTATCTTT  
 TCTCTTTCCAAGTCCACGAGAAATCAGTTTTAGTTCCATTGATGCCTACCA  
 CTCTATTACTGGTAGAAAAAGACTTGGACATCATCTCAATGGTCTGCTGGA  
 TTTCTAATATTGCCTTCTTCAGCATGTGGCCTCTATTAAAAAGAGACGGGC  
 TGGCTTTGGAATATTTTGTCTTGGAATATTGAGTAATTGGCTGATTGGAA  
 ACCTCAATTGGATTAGTAAATGGCTTGTCCTCAGTTTCTGATTCCAGGGC  
 CTACTCTCTCCAAAAAAGTTCCTAAAAGAGATACTAAAACAGTTGTTTAT  
 ACTCACTGGTTTTGGGGGTCAGTAACATTCGTTTCATACCTCGGAGCTACA  
 GTTATCCAGTTCGTAGATTGGCTGTACCTTCCACCTGCCAAGTATCCAGAT  
 TTGTGGGTTATTTTGAACACTACATTGTCGTTTGCTTGTTTCGGGTTGTTTT  
 GGCTATGGATTAACTACAATCTGTACATTTTGCGTGATTTTAAGCTTAAAG  
 ATGCTTAG

*P. pastoris* Alg6

MPHKRTPSSSLYARIPGISFENSPVDFLSPFGPAPNQWVARYIIIFAILRLAV  
 GLGSYSGFNTPPMYGDFEAQRHWMEITQHLSIEKWYFYDLQYWGLDYPPLT  
 AFHSYFFGKLGSFINPAWFALDVSRGFESVDLKSVMRATAILSELLCFIPAVIW  
 YCRWMGLNYFNQNAIEQTIIASAILFNPSLIIDHGHFQYNSVMLGFALLSILNL  
 LYDNFALAAIFFVLSISFKQMALYYSPIMFFYMLSVSCWPLKNFNLLRLATISI  
 AVLLTFATLLLPFVLVDGMSQIGQILFRVFPFSRGLFEDKVANFWCTTNILVK  
 YKQLFTDKTLTRISLVATLIAISPSCFIIFTHPKKVLLPWAFACSWAFYLSFQ  
 VHEKSVLVPLMPTTLLLVEKDLDIISMVCWISNIAFFSMWPLLKRDGLALEYF  
 VLGILSNWLIGNLNWISKWLVPFLIPGPTLSKKVPRDKTKTVVHWHFWGS  
 VTFVSYLGATVIQFVDWLYLPPAKYPDLWVILNTTLSFACFGLFWLWYNL  
 YILRDFKLKDA

FIGURE 27 (sheet 1)

*P. pastoris* ALG6 BLAST

Score	E	Sequences producing significant alignments:	(bits)	Value
gi 1420090 emb CAA99190.1	ORF YOR002w [Saccharomyces cerev...	489	e-137	
gi 7490584 pir T40396	glucosyltransferase - fission yeast ...	369	e-101	
gi 19921070 ref NP_609393.1	CG5091-PA [Drosophila melanoga...	47	4e-64	
gi 15240920 ref NP_198662.1	glucosyltransferase-like prote...	244	3e-63	
gi 7019325 ref NP_037471.1	dolichyl-P-Glc:Man9GlcNAc2-PP-d...	238	2e-61	
gi 12002040 gb AAG43163.1	AF063604.1 brain my046 protein [H...	236	7e-61	
gi 1176671 sp Q09226 ALG6 CAEEL	Probable dolichyl pyrophosph...	222	9e-57	
gi 21302638 gb EAA14783.1	agCP4617 [Anopheles gambiae str....	219	8e-56	
gi 5441788 emb CAB46771.1	probable glucosyltransferase [Sc...	192	1e-47	
gi 13129070 ref NP_076984.1	hypothetical protein MGC2840 s...	112	1e-23	
gi 2996578 emb CAA12176.1	glucosyltransferase [Homo sapiens]	112	1e-23	
gi 20835439 ref XP_131506.1	similar to Dolichyl pyrophosph...	104	3e-21	

## Alignments

*S. cerevisiae*

Score = 489 bits (1259), Expect = e-137

Identities = 274/530 (51%), Positives = 358/530 (67%), Gaps = 5/530 (0%)

Query: 20 SFENSPVDFLSPFGPAPNQWVXXXXXXXXXXXXXXXXXVGLGSYSGFNTPPMYGDFEAQRH 79  
 SF SP++DFL PF P NQW+ +GLG YSG +PP+YGDFAQRH  
 Sbjct: 16 SFYASPMYDFLYPFRPVGNQWLPEYIIFVCAVILRCTIGLGPYSGKGSPLYGDFEAQRH 75

Query: 80 WMEITQHLSIEKWYFYDLQYWGLDYPPLTAFHSYFFGKLGSFINPAWFALDVSRGFESVD 139  
 WMEITQHL + KKY+YDLQYWGLDYPPLTAFHSY G +GSF NP+WFAL+ SRGFES D  
 Sbjct: 76 WMEITQHLPLSKWYWDYDLQYWGLDYPPLTAFHSYLLGLIGSFFNPSWFALEKSRGFESPD 135

Query: 140 --LKS YMRATAILSELLCFIPAVIWCYRWMGLNYFNQNAIEQTIIASAILFNPSLIIDH 197  
 LK+YMR+T I+S++L + PAVI++ +W+G Y NQ+ I Q+I ASAILF PSL++IDH  
 Sbjct: 136 NGLKTYMRSTVVIISDILFYFPAVIYFTKWLG-RYRNQSPIGQSIASAILFQPSLMLIDH 194

Query: 198 GHFQYNSVMLGFALLSILNLLYDNFALAAIFFVLSISFKQMALYYSPIMFFYMLSVSCWP 257  
 GHFQYNSVMLG +I NLL + +A+AA+ FVLSI FKQMALYY+PI F Y+LS S  
 Sbjct: 195 GHFQYNSVMLGLTAYAINNLLDEYYAMAACVFLSICFKQMALYYAPIFFAYLLSRSL- 253

Query: 258 LKNFNLLRLATISIAVLLTFATLLLP-FVLVDGMSQIGQILFRVFPFSRGLFEDKVANFW 316  
 FN+ RL I+ A L TFA + P + L G+ I Q + R+FPF+RG+FEDKVANFW  
 Sbjct: 254 FPKFNIA RLTVIAFATLATFAII FAPLYFLGGGLKNIHQCIHRIFPFARGIFEDKVANFW 313

Query: 317 CTNINLVKYKQLFTDKTLTRISLVATLIAISPSCFIIFTHPKKVLLPWAFACSWAFYLF 376  
 C TN+ VKYK+ FT + L SL+AT+I P+ + HPKK LLP+ ACS +F+LF  
 Sbjct: 314 CVTNVVFVKYKERFTIQQLQLYSLIATVIGFLPAMIMTLLHPKKHLLPYVLIACSMSSFFLF 373

Query: 377 SFQVHEKSXXXXXXXXXXXXXKDLDIISMVCWISNIAFFSMWPLLKRDGLALEYFVLGI 436  
 SFQVHEK+ D +++S+V WI+N+A F++WPLLK+DGL L+Y V +  
 Sbjct: 374 SFQVHEKTILIPLLPITLLYSSTDWNVLSLVSWINNVALFTLWPLLKKDGLHLQYAVSFL 433

Query: 437 LSNWLIGNLNWISKWLVPFLIPGPTLSKKVKPRDTKTVVHTHWFWSVTFVSYLGVATVI 496  
 LSNWLIGN ++I+ +P L PGP++S +++++ + W S +Y+  
 Sbjct: 434 LSNWLIGNFSFITPRFLPKSLTPGPSISSINSYRRSLLPYNVVWKSFIIGTYIAMGFY 493

FIGURE 27 (sheet 2)

Query: 497 QFVDWLYLPPAKYPDLWVILNTTSLFACFGLFWLWINYLYILRDFKLKD 546  
 F+D PP+KYPDLWV+LN + F CF +FWLW Y ++ +KD  
 Sbjct: 494 HFLDQFVAPPSKYPDWVLLNCAVGFICFSIFWLWSYYKIFTSGSKSMKD 543

*S. pombe*

Score = 369 bits (946), Expect = e-101  
 Identities = 228/513 (44%), Positives = 315/513 (61%), Gaps = 35/513 (6%)

Query: 21 FEN-SPVDFLSPFGPAPNQWVXXXXXXXXXXXXXXXXXVGLGSYSGFNTPPMYGDFEAQRH 79  
 FEN +PV F+S F +++++ + +G YSG+NTPPMYGDFEAQRH  
 Sbjct: 5 FENGAPVQQFVSRFRSYSSKFLFFPCLIMSLVFMQWLISIGPYSGYNTPPMYGDFEAQRH 64

Query: 80 WMEITQHLSIEKWYFYDLQYWGLDYPLTAFHSYFFGKLGS-FINPAWFALDVSRGFESV 138  
 WME+T H + +WYF DLQ+WGLDYPLTA+ S+FFG +G F NP WFA SRGFES+  
 Sbjct: 65 WMELTLHTPVSQWYFRDLQWGLDYPLTAYVSWFFGIIGHYFFNPEWFADVTSRGFESL 124

Query: 139 DLKSYMRTAILSELLCFIPAVIWCYCRMGLNYFNQNAIEQTIIASAILFNPSLIIDHG 198  
 +LK +MR+T I S LL +P +++Y +W N +++ +LF P+L++IDHG  
 Sbjct: 125 ELKLFMRSTVIASHLLILVPPLMFYSKWSRRI--PNFVDRNASLIMVLFQPALLLIDHG 182

Query: 199 HFQYNSVMLGFALLSILNLLYDNFALAAIFEVLSISFKQMALYYSPIMFFYMLSVCWPL 258  
 HFQYN VMLG + +I NLL + + A FF L+++FKQMALY++P +FFY+L P  
 Sbjct: 183 HFQYNCVMLGLVMYAIANLLKNQYVAATFFFCLALTFKQMALYFAPPIFFYLLGTCVKPK 242

Query: 259 KNFNLLRLATISIAVLLTFATLLPFVLVDGMSQIGQILFRVFPFSRGLFEDKVANFWCT 318  
 F+ R +S+ V+ TF+ +L P++ +D + + QIL RVFPF+RGL+EDKVANFWCT  
 Sbjct: 243 IRFS--RFILLSVTVVFTFSLILFPWIYMDYKTLLPQILHRVFPFARGLWEDKVANFWCT 300

Query: 319 TNILVKYQLFDTKTLTRISLVATLIAISPCSFIIIFTHPKKVLLPWAFACSWAFYLF 378  
 N + K +++FT L ISL+ TLI+I PSC I+ F +P+K LL FA+ SW F+LFSF  
 Sbjct: 301 LNTVFKIREVFTLHQLQVISLIFTLISILPSCVILFLYPRKRLALGFASASWGFFLF 360

Query: 379 QVHEKSXXXXXXXXXXXXXKDLDIISMVCWISNIAFFSMWPLLKRDGLALEYFVLGILS 438  
 QVHEKS ++ + +N+A FS+WPLLK+DGL L+YF L ++  
 Sbjct: 361 QVHEKSVLLPLLPTSILLCHGNITTKPWIALANNLAVFSLWPLLKDKDGLGLQYFTLVLMW 420

Query: 439 NWLIGNLNWISKWLVPFLIPGPTLSKKVPKRDTKTVVHTHWFGSVTFVSYLGVATVIQF 498  
 NW IG++ SK ++ F + Y+G VI  
 Sbjct: 421 NW-IGDMVVFSKNVLF-----IQLSFYVGMIVILG 451

Query: 499 VDWLYLPPAKYPDLWVILNTTSLFACFGLFWLW 531  
 +D PP++YPDLWVILN TLSFA F +LW  
 Sbjct: 452 IDLFIPPPSRYPDLWVILNVTLSFAGFFTIYWL 484

*D. melanogaster*

Score = 247 bits (630), Expect = 4e-64  
 Identities = 175/490 (35%), Positives = 267/490 (54%), Gaps = 55/490 (11%)

Query: 57 VGLGSYSGFNTPPMYGDFEAQRHWMEITQHLSIEKWYF----YDLQYWGLDYPLTAFHS 112  
 + L SYSGF++PPM+GD+EAQRHW EIT +L++ +WY DLQYWGLDYPLTA+HS  
 Sbjct: 19 ISLYSYSGFDSPPMHGDYEAQRHWQEITVNLA VGEWYTNSSNNDLQYWGLDYPLTAYHS 78

Query: 113 YFFGKLGSFINPAWFALDVSRGFESVDLKSYMRTAILSELLCFIPAVIWCYCRMGLNYF 172  
 Y G++G+ I+P + L SRGFES + K +MRAT + +++L ++PA++ + +  
 Sbjct: 79 YLVGRIGASIDPRFVELHKS RGFESKEHKRFMRATVVSADVLIYLPAMLLLAYSLDKAFR 138

FIGURE 27 (sheet 3)

Query: 173 NQNAIEQTIIASAILFNPSLIIIDHGHFQYNSVMLGFALLSILNLLYDNFALAAIFFVLS 232  
 + + + + +A P +ID+GHFQYN++ LGFA ++I +L F AA FF L+  
 Sbjct: 139 SDDKLFLLFTLVAAAY---PGQTLIDNGHFQYNNISLGFAAVAI AAILRRRFYAAAFFFTLA 195

Query: 233 ISFKQMALYYSPIMFFYMLSVCWPLKNFN--LLRLATISIAVLLTFATLLLPPFVLVDGM 290  
 +++KQM LY+S + FF L C K+F + ++ I+ VL TFA L +P+ + +  
 Sbjct: 196 LNYKQMELYHS-LPFFAFLLGECVSQKSFASFIAEISRIA AAVVLGTFAILWVPW--LGSL 252

Query: 291 SQIGQILFRVFPFSRGLFEDKVANFWCTTNILVKYKQLFTDKTLTRISLVATLIAISPSC 350  
 + Q+L R+FP +RG+FEDKVAN WC N++ K K+ ++ + + + TLIA P+  
 Sbjct: 253 QAVLQVLHRLFPVARGVFEDKVANVWCAVNVVWKLKHHISNDQMALVCIAC TLIASLPTN 312

Query: 351 FIIFTHPKKVLLPWAFACSWAFYLF SFQVHEKSXXXXXXXXXXXXXKDLDIISMVCW- 409  
 ++F V A S AF+LFSFQVHEK+ + + CW  
 Sbjct: 313 VLLFRRRTNVGFLALFNTSLAFFLFSFQVHEKTILLTALPA-----LFLKWCWP 362

Query: 410 -----ISNIAFFSMWPLLKRDLGLALEYFVLGILSNWLIGNLNWISKWLVP SFLIPGPTLS 464  
 + FSM PLL RD L + V + + + + SK LS  
 Sbjct: 363 DEMILFLEVTVFSMLPLLARDELLVPAVVATVAFHLIFKCFDSKSK-----LS 410

Query: 465 KKVPKRDTKTIVHTHWFGSVTFVSYLGA TVIQFVDWLYLP-PAKYPDLWVILNTTSLFA 523  
 + P + + + + +S + A+ L +P P KYPDLW ++ + S  
 Sbjct: 411 NEYPLKYIANI-----SQILMISVVVAS-----LTPAPTKYPDLWPLIISVTSCG 456

Query: 524 CFGLFWLWIN 533  
 F LF+LW N  
 Sbjct: 457 HFFLFFLWGN 466

## A. thaliana

Score = 244 bits (622), Expect = 3e-63  
 Identities = 187/488 (38%), Positives = 248/488 (50%), Gaps = 39/488 (7%)

Query: 62 YSGFNTPPMYGDFEAQRHWMEITQHLSIEKWY----FYDLQYWGLDYPPLTAFHSYFFGK 117  
 YSG PP +GDFEAQRHWMEIT +L + WY + DL YWGLDYPPLTA+ SY G  
 Sbjct: 61 YSGAGIPPKFGDFEAQRHWMEITTNLPVIDWYRNGTYNDLTYWGLDYPPLTAYQSYIHGI 120

Query: 118 LGSFINPAWFALDVSRGFESVDLKS YMRATAILSELLCFIPAVI WYCRWMGLNYFNQNAI 177  
 F NP AL SRG ES K MR T + S+ F PA +++ N  
 Sbjct: 121 FLRFFNPESVALLSSRGHESYLGKLLMRWTVLSSDAFIFFPAALFFVLVYHRNRTRGGKS 180

Query: 178 EQTIIASAILFNPSLIIIDHGHFQYNSVMLGFALLSILNLLYDNFALAAIFFVLSISFKQ 237  
 E + IL NP LI+IDHGHFQYN + LG + +I +L ++ L + F L++S KQ  
 Sbjct: 181 EVAWHIAMILLNPCLILIDHGHFQYNCISLGLTVGAIAAVLCESEVLTCVLFSLALSHKQ 240

Query: 238 MALYYSPIMFFYMLSVCWPLKNFNLLRLATISIAVLLTFATLLLPPFVLVDGMSQIGQIL 297  
 M+ Y++P F ++L C K+ +L + + IAV++TF P+ V + +L  
 Sbjct: 241 MSAYFAPAFFSHLLG-KCLRRKS-PILSVIKLGIAVIVTFVIFWWPY--VHSLDDFLMVL 296

Query: 298 FRVFPFSRGLFEDKVANFWCTTNILVKYKQLFTDKTLTRISLVATLIAISPSCFIIFTHP 357  
 R+ PF RG++ED VANFWCTT+IL+K+K LFT ++L ISL AT++A PS P  
 Sbjct: 297 SRLAPFERGIYEDYVANFWCTTSILIKWKNLFTTQSLKSISLAATILASLPSMVQQILSP 356

Query: 358 KKVLLPWAFACSWAFYLF SFQVHEKSXXXXXXXXXXXXXKDLDIISMVCWISNIAFFS 417  
 + S AFYLF SFQVHEKS L + ++ A FS  
 Sbjct: 357 SNEGFLYGLLNSSMAFYLF SFQVHEKSILMPFLSATLLA----LKLDPHFHSHLTYYALFS 412

## FIGURE 27 (sheet 4)

Query: 418 MWPLLKRDGLALEYFVLGILSNWLI---GNLNWISKWLVP SFL---IPGPTLSKKVPKRD 471  
M+PLL RD L + Y L L + GN + I K V F PG  
Sbjct: 413 MFPLLCRDKLLIPYLTLSFLFTVIYHSPGNHHAIQKTDVSFFSFKNFPGYVF----- 464

Query: 472 TKTVVHTHWFWSVTFVSYLGATVIQFVDWLYLPPAKYPDLWVILNTTLSFACFGLFWLW 531  
++ TH+F V V YL PP KYP L+ L L F+ F +F +  
Sbjct: 465 ---LLRTHFFISVVLHVLYLTIK-----PPQKYPFLFEALIMILCFSYFIMFAFY 511

Query: 532 INYNLYIL 539  
NY + L  
Sbjct: 512 TNYTQWTL 519

FIGURE 28

*K. lactis* ALG6

ATCTCTGTTTCAACAGCTCTTGCATTCAATTGGTTCTTTTCGGTCCAATCTATA  
TCTTTGGAGGATACAAGAAGCTTAGTGCAATCAATGCACAGGATTTTTCCAT  
TTGCCAGGGGTATCTTTGAAGATAAAGTTGCGAATTTTTGGTGCGTTTCTA  
ATATTTTCATCAAATATAGAAATCTATTCCTCAGAAGGATCTTCAATTAT  
ACTCATTACTCGCAACAGTTATTGGGCTTTTACCATCATTCAATTATAACAT  
TTTTATACCCGAAGAGACATTTACTACCATATGCTTTGGCCGCATGTTTCGA  
TGTCATTCTTCTTATTAGCTTCCAGGTTTCATGAAAAGACAATCTTATTAC  
CTTTACTTCCTATTACACTCTTGTACACGTCAAGAGATTGGAATGTTCTAT  
CATTGGTTTGTGGATTAACAACGTGGCATTGTTTACACTCTGGCCATTAC  
TGAAAAAGGACAATCTAGTATTGCAATATGGAGTCATGTTTCATGTTTAGC  
AATTGGTTGATCGGTAACCTTCAGTTTCGTACACACCACGCTTCCTCCCAAAA  
TTTTTGACACCAGGGCCATCCATCAGTGATATAGATGTTGATTATAGACGG  
GCAAGTTTACTACCCAAGAGCCTAATATGGAGATTAATCATTGTTGGCTCA  
TATATTGCAATGGGGATTATTCATTTTCTAGACTATTACGTCTCCCCGCCA  
TCAAAATACCCTGATTTATGGGTGCTTGCCAATTGTTCTTGGGCTTCTCA  
TGTTTTGTGACATTTTGGATATGGAACAATTATAATTATTCGAAATGAGAA  
ACAGCACTTTGCAAGATTTA

*K. lactis* Alg6p

ISVSTALAFIGSFGPIYIFGGYKNLVQSMHRIFPFARGIFEDKVANFWCVSNIFIK  
YRNLFTQKDLQLYSLLATVIGLLPSFIITFLYPKRHLLPYALAACSMSSFLLFSFQ  
VHEKTILLPLLPITLLYTSRDWNVLSLVCWINNVALFTLWPLLKKDNLVLQYG  
VMFMFSNWLIGNFSFVTPRFLPKFLTPGPSISDIDVDYRRASLLPKSLIWRLIIV  
GSYIAMGIIHFLDYVSPPSKYPDLWVLANCSLGFSCFVTFWIWNNYNYSKZE  
TALCKI

FIGURE 29 (sheet 1)

*K. lactis* ALG6 BLAST

Score E  
Sequences producing significant alignments: (bits) Value

gi 1420090 emb CAA99190.1	ORF YOR002w [Saccharomyces cerev...	392	e-108
gi 7490584 pir T40396	glucosyltransferase - fission yeast ...	187	2e-46
gi 15240920 ref NP_198662.1	glucosyltransferase-like prote...	117	2e-25
gi 7019325 ref NP_037471.1	dolichyl-P-Glc:Man9GlcNAc2-PP-d...	103	2e-21
gi 12002040 gb AAG43163.1	AF063604.1 brain my046 protein [H...	102	8e-21
gi 19921070 ref NP_609393.1	CG5091-PA [Drosophila melanoga...	101	1e-20

## Alignments

*S. cerevisiae*

Score = 392 bits (1006), Expect = e-108  
Identities = 182/280 (65%), Positives = 218/280 (77%), Gaps = 1/280 (0%)  
Frame = +1

```

Query: 1   ISVSTALAFIGSFGPIYIFGG-YKNLVQSMHRIFPFARGIFEDKVANFWCVSNIFIKYRN 177
          I+ +T   F   F P+Y   GG   KN+ Q +HRIFPFARGIFEDKVANFWCV+N+F+KY+
Sbjct: 265 IAFATLATFAIIFAPLYFLGGGLKNIHQCIHRIFPFARGIFEDKVANFWCVTNVFKYKE 324

Query: 178 LFTQKDLQLYSLLATVIGLLPSFIITFLYPKRHLLPYALACSMSFFLFSFQVHEKXXXX 357
          FT + LQLYSL+ATVIG LP+ I+T L+PK+HLLPY L ACSMSFFLFSFQVHEK
Sbjct: 325 RFTIQQLQLYSLIATVIGFLPAMIMTLLHPKKHLLPYVLIACSMSFFLFSFQVHEKTILI 384

Query: 358 XXXXXXXXXYSRDWNVLSLVCSWINNVALFTLWPLLKKDNLVLQYGVFMFMSNWLIGNFSF 537
          Y+S DWNVLSLV WINNVALFTLWPLLKKD L LQY V F+ SNWLIGNFSF
Sbjct: 385 PLLPITLLYSSTDWNVLSLVSWINNVALFTLWPLLKKDGLHLQYAVSFLLSNWLIGNFSF 444

Query: 538 VTPRFLPKFLTPGPSISDIDVDYRRASLLPKSLIWRLIIVGSYIAMGIIHFLDYVSPPS 717
          +TPRFLPK LTPGPSIS I+ DYRR SLLP +++W+ I+G+YIAMG HFLD +V+PPS
Sbjct: 445 ITPRFLPKSLTPGPSISSINSIDYRRSLLPYNVVWKSFIIGTYIAMGFYHFLDQFVAPPS 504

Query: 718 KYPDLWVLANCSLGFSCFVTFWIWNXYLFEMRNSTLQDL 837
          KYPDLWVL NC++GF CF FW+W+ Y +F + +++DL
Sbjct: 505 KYPDLWVLLNCAVGFIKFSIFWLWSYKIFTSGSKSMKDL 544

```

*S. pombe*

Score = 187 bits (475), Expect = 2e-46  
Identities = 106/280 (37%), Positives = 150/280 (53%), Gaps = 1/280 (0%)  
Frame = +1

```

Query: 1   ISVSTALAFIGSFGPIYIFGGYKNLV-QSMHRIFPFARGIFEDKVANFWCVSNIFIKYRN 177
          +SV+   F   P +I+ YK L+ Q +HR+FPFARG++EDKVANFWC N   K R
Sbjct: 251 LSVTVVFTFSLILFP-WIYMDYKTLLPQILHRVFPFARGLWEDKVANFWCTLNTVFKIRE 309

Query: 178 LFTQKDLQLYSLLATVIGLLPSFIITFLYPKRHLLPYALACSMSFFLFSFQVHEKXXXX 357
          +FT LQ+ SL+ T+I +LPS +I FLYP++ LL A+ S FFLFSFQVHEK
Sbjct: 310 VFTLHQLQVISLIFTLISILPSCVILFLYPRKRLALGFASASWGFFLFSFQVHEKSVLL 369

```

FIGURE 29 (sheet 2)

Query: 358 XXXXXXXXYTSRDWNVLSLVCWINNVALFTLWPLLKKDNLVLQYGVFMFMSNWLIGNFSF 537  
 + + NN+A+F+LWPLLKKD L LQY + + NW  
 Sbjct: 370 PLLPTSILLCHGNITTKPWIALANNLAVFSLWPLLKKDGLGLQYFTLVLMWNW----- 422

Query: 538 VTPRFLPKFLTTPGPSISDIDVDYRRASLLPKSLIWRLIIVGSYIAMGIIHFLDYVSPPS 717  
 I D+ V K++++R I + Y+ M +I +D ++ PPS  
 Sbjct: 423 -----IGDMVV-----FSKNVLFRFIQLSFYVGMIVILGIDLFIPPPS 460

Query: 718 KYPDLWVLANCSLGFSCFVTFWIWNNYXLFEMRNSTLQDL 837  
 +YPDLWV+ N +L F+ F T ++W L + + DL  
 Sbjct: 461 RYPDLWVILNVTLSFAGFFTIYLTWTLGRLLHISKLSTDL 500

*A. thaliana*

Score = 117 bits (292), Expect = 2e-25  
 Identities = 81/240 (33%), Positives = 120/240 (50%), Gaps = 2/240 (0%)  
 Frame = +1

Query: 85 MHRIFPFARGIFEDKVANFWCVSNIFIKYRNLFTQKDLQLYSLLATVIGLLPSFIITFLY 264  
 + R+ PF RGI+ED VANFWC ++I IK++NLFT + L+ SL AT++ LPS + L  
 Sbjct: 296 LSRLAPFERGIYEDYVANFWCTTSILIKWKNLFTTQSLKSISLAATILASLPSMVQQILS 355

Query: 265 PKRHLLPYALAACSMSSFFLFSFQVHEKXXXXXXXXXXXXXYTSRDWNVLSLVCWINNVALF 444  
 P Y L SM+F+LFSFQVHEK + L + ALF  
 Sbjct: 356 PSNEGFLYGLLNSSMAFYLFSSFQVHEKSILMPFLSATLLALKLPDHFSLHTYY----ALF 411

Query: 445 TLWPLLKKDNLVLQYGVFMFMSNWLIGNFSFVTPRFLPKFLTTPG--PSISDIDVDYRRAS 618  
 +++PLL +D L++ Y + SF+ F + +PG +I DV +  
 Sbjct: 412 SMFPLLCRDKLLIPYLT-----SFL---FTVIYHSPGNHHAIQKTDVSFFSFK 457

Query: 619 LLPKSLIWRLIIVGSYIAMGIIHFLDYVSPPSKYPDLWVLANCSLGFSCFVTFWIWNNY 798  
 P + L+ +I++ ++H L + PP KYP L+ L FS F+ F + NY  
 Sbjct: 458 NFPGYVF--LLRTHFFISV-VLHVLYLTIKPPQKYPFLFEALIMILCFSYFIMEFYTN 514

*H. sapiens*

Score = 103 bits (258), Expect = 2e-21  
 Identities = 78/266 (29%), Positives = 123/266 (46%), Gaps = 3/266 (1%)  
 Frame = +1

Query: 7 VSTALAFIGSFGPIYI--FGGYKNLVQSMHRIFPFARGIFEDKVANFWCVSNIFIKYRNL 180  
 V A + SF ++ F + +Q + R+FP RG+FEDKVAN WC N+F+K +++  
 Sbjct: 232 VKLACIVVASFVLCWLPFFTEREQTLQVLRRLFPVDRGLFEDKVANIWCSENVFLKIKDI 291

Query: 181 FTQKDLQLYSLLATVIGLLPSFIITFLYPKRHLLPYALAACSMSSFFLFSFQVHEKXXXXX 360  
 + + S T + LLP+ I L P + L +C++SFFLFSFQVHEK  
 Sbjct: 292 LPRHIQLIMSFCFTFLSLLPACIKLILQPSKGFKFTLVSCALSFFLFSFQVHEKSILLV 351

Query: 361 XXXXXXXXYTSRDWNVLSLVCWINNVALFTLWPLLKKDNLVLQYGVFMF--FSNWLIGNFSF 537  
 + + + W V+ F++ PLL KD L++ V M F + +FS  
 Sbjct: 352 SLPVCLVLS---EIPFMSTWFLLVSTFSMLPLLKDELLMPSVVTMAFFIACVTSFSI 407

Query: 538 VTPRFLPKFLTTPGPSISDIDVDYRRASLLPKSLIWRLIIVGSYIAMGIIHFLDYVSPPS 717  
 + SIS V S I + + + S I M ++ + + PP  
 Sbjct: 408 FEKTSEEELQLKSFSIS---VRKYLPCFTFLSRIIQYLFLISVITMVLTLTMTVTLDP 464

Query: 718 KYPDLWVLANCSLGFSCFVTFWIWNN 795  
 K PDL+ + C + F+ F ++ N  
 Sbjct: 465 KLPDLFSVLVCFVSCNLNFFLVYFN 490



FIGURE 30

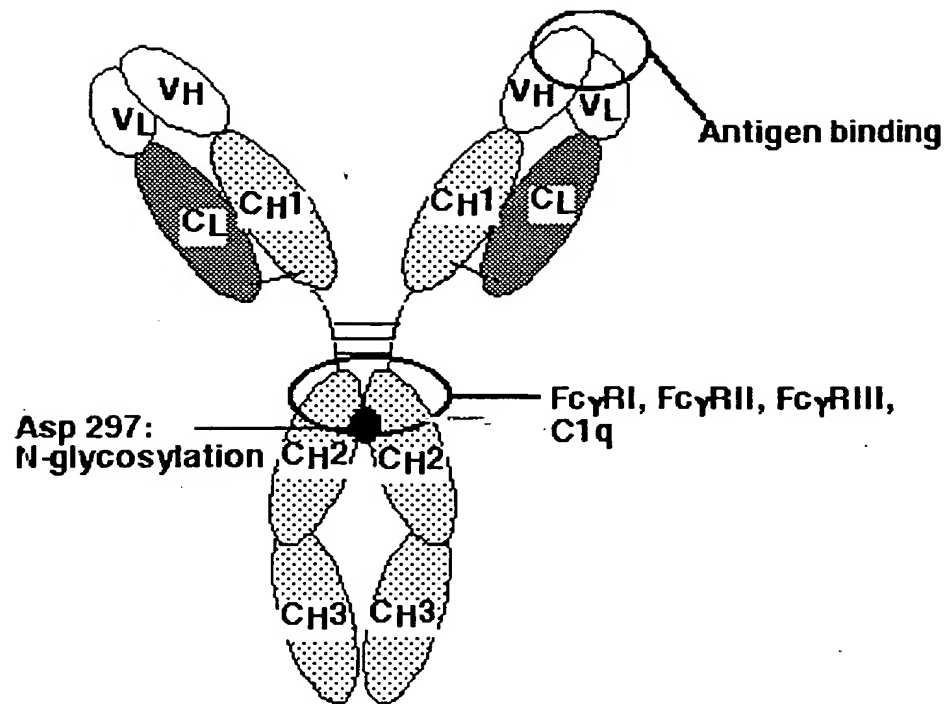


FIGURE 31

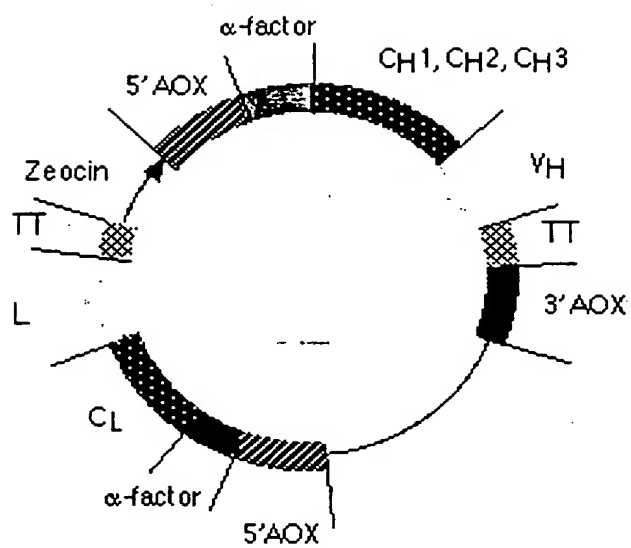


FIGURE 32

>gi|6754685|ref|NM\_010795.1| Mus musculus mannoside acetyl  
glucosaminyltransferase 3 (Mgat3), mRNA

ATGAAGATGAGACGCTACAAGCTCTTTCTCATGTTCTGTATGGCTGGCCTGTGCCTCATATCCTTCCTGC  
ACTTCTTTAAGACCTTATCCTATGTACCTTCCCGAGAGAACTGGCCTCCCTCAGCCCTAACCTCGTATC  
CAGCTTCTTCTGGAACAATGCCCCGTGCTACTCCCCAGGCCAGTCCGGAGCCGGGTGGCCCCGACCTATTG  
CGGACACCCCTCTACTCCCACTCTCCCTGCTCCAGCCACTGTCCCCGAGCAAGGCCACAGAGGAACTGC  
ACCGGGTGGACTTCGTGTTGCCGGAGGACACACGGAGTATTTGTGCGCACCAAGCTGGTGGTGTGTG  
CTTCAAACCAAGGTACCAGGATGCTGGAGAAACCTTCGCCAGGGCGGACAGAGGAGAAGCCCCGAAGTGTCT  
GAGGGCTCCTCAGCCCCGGGGACCTGCTCGGAGGCCCATGAGGCACGTGTTGAGTACGCGGGAGCGCCTGG  
GCAGCCGGGGCACTAGGCGCAAGTGGGTTGAGTGTGTGTGCTGCCAGGCTGGCACGGGGCCAGTTGCGG  
GGTGGCCACGGTGGTGCAGTATTCCAACCTGCCACCAAGGAACGCCTGGTACCCAGGGAGGTACCGAGG  
CGGGTTATCAACGCCATCAACATCAACCACGAGTTCGACCTGCTGGATGTGCGCTTCCATGAGCTGGGAG  
ATGTTGTGGACGCCTTCGTGGTCTGTGAATCTAATTTACCCGCTACGGGGAGCCTCGGCCGCTCAAGTT  
CCGAGAGATGCTGACCAATGGCACCTTCGAGTACATCCGCCACAAGGTGCTCTATGTCTTCCTGGACCAT  
TTCCACCTGGTGGCCGTGAGGACGGCTGGATTGCGGATGACTACCTGCGCACCTTCCTACCCAGGATG  
GCGTCTCCCGCCTGCGCAACCTGCGGCCCGATGACGTCTTTATCATCGACGATGCGGACGAGATCCCTGC  
GCGTGATGGTGTGCTGTTCTCAAACCTCTACGATGGCTGGACAGAGCCCTTCGCCTTCCACATGCGGAAG  
TCCCTGTATGGTTTCTTCTGGAAGCAGCCGGGCACACTGGAGGTGGTGTGAGGCTGCACCATGGACATGC  
TGCAGGCCGTGTATGGGCTGGATGGCATCCGCCTGCGCCGCCAGTACTACACCATGCCCAACTTCCG  
GCAGTATGAGAACCACCGCCACATCCTAGTGCAGTGGTCTCTCGGCAGCCCCCTGCACTTCGCGGGC  
TGGCATTGCTCCTGGTGTCTTACACCCGAGGGCATCTACTTTAAACTCGTGTGAGCCAGAAATGGCGACT  
TCCCCCGCTGGGGTGACTATGAGGACAAGAGGGACCTCAATTACATCCGCAGCTTGATCCGCACTGGGGG  
ATGGTTTCGACGGAACGCAGCAGGAGTACCCTCCTGCGGACCCAGTGAGCACATGTATGCTCCTAAATAC  
CTGCTCAAGAACTATGACCAGTTCCGCTACTTGCTGGAAAATCCCTACCGGGAGCCCCAAGAGCACTGTAG  
AGGGTGGGCGCCAGAACCAGGGCTCAGATGGAAGGCCATCTGCTGTCAGGGGCAAGTTGGATACAGTGGA  
GGGCTAG

>gi|2117717|pir||JC4362 beta-1,4-mannosyl-glycoprotein 4-beta-N-  
acetylglucosaminyltransferase (EC 2.4.1.144) III - mouse  
MRRYKLFMLFCMAGLCLISFLHFFKTLSTVTFPRELASLSPNLISFFWNNAPVTPQASPEPGDPDLLRT  
PLYSHSPLLQPLSPSKATEELHRVDFVLPEDTTEYFVRTKAGGVCFKPGTRMLEKPSGRTEEEKTEVSEG  
SSARGPARRPMRHLSSRERLGSRGTRRKWVECVCLPGWHGPSCGVPTVVQYSNLPKTERLVPREVPRRV  
INAININHEFDLLDVRFHGELGDVVDFAFVVCDSNFTAYGEPRLKFRMLTNGTFEYIRHKVLYVFLDHFP  
PGGRQDGWIADDYLRTFLTQDGVSRRLRNLRPDDVFIIDDADEIPARDGVLFLKLYDGTWTEPF AFHMRKSL  
YGF FWKQPGTLEV VSGCTMDMLQAVYGLDGI RLRRRQYYT MPNFRQYENRTGHILVQWSLGSPLHFAGWH  
CSWCFTPEGIYFKLVSAQNGDFPRWGDYEDKRD LNYIRSLIRTGGWFDGTQQEYPPADPSEHMYAPKYL  
KNYDQFRYLL ENPYREP KSTVEGGRQNQGS DGRSSAVRGKLDTAEG

FIGURE 33

>gi|6912501|ref|NM\_012214.1| Homo sapiens mannosyl  
(alpha-1,3-)-glycoprotein beta-1,4-N-  
acetylglucosaminyltransferase, isoenzyme A (MGAT4A), mRNA

GAAATGAACCTCTCTTATTGATTTTTATTGGCCTAGAGCCAGGAGTACTGCATTTCAGTTGACTTTCAGG  
GTAAAAAGAAAACAGTCCTGGTTGTTGTCATCATAAACATATGGACCAGTGTGATGGTGAAATGAGATG  
AGGCTCCGCAATGGAAGTGTAGCCACTGCTTTAGCATTATCACTTCCTTCCTTACTTTGTCTTGGTAT  
ACTACATGGCAAAATGGGAAAGAAAAAAGTATTGCTTATCAACGAGAATTCCTTGCTTTGAAAGAACGT  
CTTCGAATAGCTGAACACAGAATCTCACAGCGCTCTTCTGAATTAATACGATTGTGCAACAGTTCAAG  
CGTGTAGGAGCAGAAACAAATGGAAGTAAGGATGCGTTGAATAAGTTTTTCAGATAATACCCTAAAGCTG  
TTAAAGGAGTTAACAAGCAAAAAATCTCTTCAAGTGCCAAAGTATTTATTATCATTTGCCTCATTATTTG  
AAAAATGAAGGAAGTCTTCAACCTGCTGTACAGATTGGCAACGGAAGAACAGGAGTTTCAATAGTCATG  
GGCATTCCCACAGTGAAGAGAGAAGTTAAATCTTACCTCATAGAACTCTTCATTCCCTTATTGATAAC  
CTGTATCCTGAAGAGAAGTTGGACTGTGTTATAGTAGTCTTCATAGGAGAGACAGATATTGATTATGTA  
CATGGTGTGTAGCCAACCTGGAGAAAGAATTTCTAAAGAAATCAGTTCTGGCTTGGTGGAAGTCATA  
TCACCCCTGAAAGCTATTATCCTGACTTGACAAACCTAAAGGAGACATTTGGAGACTCCAAAGAAAGA  
GTAAGATGGAGAACAAAGCAAAACCTAGATTACTGTTTTCTAATGATGTATGCTCAAGAAAAGGGCATA  
TATTACATTTCAGCTTGAAGATGATATTATTGTCAAACAAAATTATTTTAATACCATAAAAAATTTGCA  
CTTCAACTTTCTTCTGAGGAATGGATGATTCTAGAGTTTTCCAGCTGGGCTTCATTGGTAAAATGTTT  
CAAGCGCCGGATCTTACTCTGATTGTAGAATTCATATTGTTTACAAGGAGAAACCCATTGATTGG  
CTCCTGGACCATATTCTCTGGGTGAAAGTCTGCAACCCTGAAAAAGATGCAAAACATTGTGATAGACAG  
AAAGCAAATCTGCGAATTCGCTTCAGACCTTCCCTTTTCCAACATGTTGGTCTGCACTCATCACTATCA  
GGAAAAATCCAAAACTCACGGATAAAGATTATATGAAACCATTACTTCTTAAATCCATGTAAACCCA  
CCTGCGGAGGTATCTACTTCCTTGAAGGTCTACCAAGGGCATACGCTGGAGAAAACCTACATGGGAGAG  
GATTTCTTCTGGGCTATCACACCGATAGCTGGAGACTACATCTTGTTTAAATTTGATAAACAGTCAAT  
GTAGAAAGTTATTTGTTCCATAGCGGCAACCAAGAACATCCTGGAGATATTCTGCTAAACACAACCTGTG  
GAAGTTTTGCCTTTTAAGAGTGAAGGTTTGGAAATAAGCAAAGAAACCAAGACAAACGATTAGAAGAT  
GGCTATTTTCAAGATAGGAAATTTGAGAATGGTGTGTCAGAAAGGAATGGTGGATCCCAAGTCTCAATCCC  
ATTTTCAGCCTTTTCGACTTTTCAGTTATTTCAGAATTCTGCTGTTTGGGCCATTCTTAATGAGATTTCATATT  
AAAAAAGCCACCAACTGATCATCTGAGAAACCAACACATTTTTTCTGTGAATTTGTTAATTAAAGATA  
GTTAAGCATGTATCTTTTTTTTATTCTACTTGAACACTACCTCTTGTGAAGTCTACTGTAGATAAGAC  
GATTGTCATTTCCACTTGGAAAGTGAATCTCCCATATAAATTGTATTTGTTTGAAACTAAGCTGTCCTC  
AGATTTTAACCTGACTCAAACATTTTTCAATTATGACAGCCTGTTAATATGACTTGTACTATTTTGTA  
TTATACTAATAACATAAGAGTTGTACATATTGTTACATTCTTTAAATTTGAGAAAACTAATGTTACATA  
CATTTTATGAAGGGGTACTTTTGAGGTTCACTTATTTTACTATT

>gi|6912502|ref|NP\_036346.1| mannosyl (alpha-1,3-)-  
glycoprotein beta-1,4-N-acetylglucosaminyltransferase,  
isoenzyme A; UDP-N-acetylglucosamine:alpha1,3-d-mannoside  
beta1,4-N-acetylglucosaminyltransferase; alpha-1,3-  
mannosyl-glycoprotein beta-1,4-N-  
acetylglucosaminyltransferase [Homo sapiens]

MRLRNGTVATALAFITSFLTLSWYTTWQNGKEKLIAYQREFLALKERLRIAEHRISQ  
RSSELNTIVQQFKRVGAETNGSKDALNKFSDNTLKLKELTSKKSQVPSIYYHLPH  
LLKNEGSLQPAVQIGNRTGVSIVMGIPTVKREVKSyliETLHSLIDNLYPEEKLD  
VIVVFIGETDIDYVHGVVANLEKEFSKEISSGLVEVISPPESYYPDLTNLKETFGDS  
KERVWRWKQNLDYCFLLMYAQEKGIYYIQLEDDIIVKQNYFNTIKNFALQLSSEEW  
MILEFSQLGFIGKMFQAPDLTLIVEFIFMFYKEKPIDWLLDHILWVKVCNPEKDAKH  
CDRQKANLRIRFRPSLFQHVGLHSSLSGKIQKLTDKDYMKPLLLKIHVNPPAEVSTS  
LKVYQGHTLEKTYMGEDFFWAITPIAGDYILFKFDKPVNVESYLFHSGNQEHPGDIL  
LNTTVEVLPFKSEGLEISKETDKRLEDGYFRIGKFENGVAEGMVDPSLNPI SAFRL  
SVIQNSAVWAILNEIHIKKATN

FIGURE 34 (sheet 1)

>gi|18997006|gb|AF474154.1| Mus musculus N-acetylglucosaminyltransferase V (Mgat5) mRNA, complete cds

ATTGCTAGAGAGAGATGGCTTTCTTTTCTCCCTGGAAGTTGTCCTCTCAGAAGCTGG  
GCTTTTTCTCTGGTGACTTTCGGCTTCATCTGGGGCATGATGCTTCTGCACTTCACCA  
TCCAGCAGCGGACTCAGCCCGAGAGCAGCTCCATGTTACGGGAGCAGATCCTTGACC  
TCAGCAAGAGGTACATTAAGGCACTGGCAGAGGAGAACAGGGACGTGGTGGATGGCC  
CCTACGCTGGTGTTCATGACAGCCTATGATCTGAAGAAAACGCTCGCCGTCTTGCTGG  
ATAACATCCTGCAGCGCATTGGCAAGCTCGAGTCAAAGGTGGACAATCTGGTCAACG  
GCACAGGAGCGAACTCCACCAACTCCACCACGGCTGTCCCCAGCTTGGTGTGCGCTTG  
AGAAAATTAATGTGGCAGATATCATTAAATGGAGTTCAGGAAAAATGTGTATTGCCTC  
CTATGGATGGCTACCCCCACTGCGAGGGGAAAATCAAGTGGATGAAGGACATGTGGC  
GCTCGGACCCCTGCTACGCAGACTATGGAGTGGACGGGACCTCCTGCTCCTTTTTTA  
TTTACCTCAGTGAGGTTGAAAATTGGTGTCTCGTTTACCTTGGAGAGCAAAAAATC  
CCTATGAAGAAGCTGATCATAACTCATTGGCGGAAATCCGTACGGATTTTAACATTTC  
TCTACGGCATGATGAAGAAGCACGAGGAGTTCCGTTGGATGAGGCTTCGGATCCGGC  
GAATGGCTGACGCGTGGATCCAAGCTATCAAGTCTCTGGCGGAGAAACAAAACCTTG  
AGAAGAGGAAACGGAAGAAAATCCTTGTTACCTGGGGCTCCTGACCAAGGAATCGG  
GCTTCAAGATTGCGGAGACAGCATTTCAGCGGTGGCCCTCTGGGTGAACTCGTTCAGT  
GGAGTGACTTAATCACATCTCTGTACCTGCTGGGCCATGACATCCGGATCTCGGCCT  
CACTGGCTGAGCTCAAGGAGATAATGAAGAAGGTTGTTGGAAACCGGTCTGGCTGTC  
CAACTGTAGGAGACAGAATCGTTGAGCTGATTTATATCGATATTGTGGGACTTGCTC  
AATTTAAGAAAACACTAGGGCCATCCTGGGTTTATTACCAGTGCATGCTCCGGGTGC  
TAGACTCCTTTGGAACAGAACCTGAGTTCAATCATGCGAGCTATGCCAGTCAAAAG  
GCCACAAGACCCCTGGGGAAAGTGAATCTGAACCCGCAGCAGTTTTACACCATGT  
TCCCTCATACCCAGACAACAGCTTTCTGGGCTTCGTGGTGGAGCAGCACCTGAACT  
CCAGCGACATTACACCATCAACGAGATCAAAAGGCAGAACCCAGTCCCTTGTGTATG  
GCAAAGTGGATAGTTTCTGGAAGAATAAGAAAATCTACCTGGATATCATTACACGT  
ACATGGAAGTGCACGCCACTGTTTATGGCTCCAGTACCAAGAACATTCCCAGTTACG  
TGAAAACCATGGCATTCTCAGTGGACGTGACCTGCAGTTTCTTCTCCGGGAAACCA  
AGCTGTTCTGTTGGGCTCGGATTCCCTTATGAAGGCCAGCTCCCTTGGAGGCCATCG  
CGAATGGATGTGCTTCTCTGAACCCCAAGTTCAACCCTCCCAAAGCAGCAAAAACA  
CAGACTTCTTCATTGGCAAGCCAACACTGAGAGAGCTGACATCCCAGCATCCTTACG  
CAGAAGTCTTCATCGGCCGGCCACACGTCTGGACTGTGGATCTCAATAACCGAGAGG  
AAGTAGAAGATGCAGTAAAAGCCATCTTAAACCAGAAGATTGAGCCGTATATGCCAT  
ATGAGTTCACATGTGAAGGCATGCTGCAGAGAATCAACGCTTTTATTGAAAAACAGG  
ACTTCTGCCATGGCCAAGTGATGTGGCCGCCCCCTCAGCGCCCTGCAGGTTAAGCTGG  
CTGAGCCAGGGCAGTCTTGCAAACAGGTGTGCCAGGAGAGCCAGTCTATCTGCGAGC  
CATCCTTCTTTCAACACCTCAACAAGGAAAAGGACCTGCTGAAGTATAAGGTGACCT  
GCCAAAGCTCAGAACTGTACAAGGACATCCTGGTGCCCTCCTTCTACCCCAAGAGCA  
AGCACTGTGTGTTCCAAGGGGACCTCCTGCTCTTCAGTTGTGCGGAGCCCATCCCA  
CACACCAGCGGATCTGCCCCCTGCCGGGACTTCATCAAGGGCCAAGTGGCCCTCTGCA  
AAGACTGCCTATAGCATCGCTGCCCTGAATTAACCTCAGACGGGAAAGACGTGGCTCC  
ACTGGGCAGGGCCAAGGGGCACAAAGACATTCAGGGACTCTGACCAGAGCCTGAGAT  
CTTTGGTCCAGGGCTTGAGTTTAGTACCGCTCCAGCCACAGCCAGTGCATCCCAGTT  
TACACCAAACCAAGGGAACAGGTTAGAACAGGAACCTGGGTCTCCTCAGTGTA  
AGGAATGTCCTCTCTGTCTGGGAGATCGAGCGACTGTAGGGAAAGGATCCAGGCAGT  
TGCTCCCGGGAATTTTTTTTTTTTTTTTTTTTAAAGAAGGGATAAAAGTCCCGAGAC

TCATTCAAACCTGAAAACAAAACAGGAAGAGGGAATTGAGCCAATTGGGAAGGACTTT  
GGGGCCGATCCTAAACCAATTAATTTATTTATTTGGGAGGATGGGGGCGGGCTCGGG  
AGGGAGGAGAGGGGTTGAACAGTTTCCTTTTGTTCCTCACTGTTAATTCGCCCACCT  
TCGGGCCCTTCTTGTTCCTGCAGCGCCAAGCAGGGTGCAGAGGGGCTGTGGCTTGCTT  
GAGGGGCCACTGTGGGGCTTCACTCCTGGTCACAGGTGGCAGCAGAGAAAAGAGATG  
TCTATAAGCAGGGGGATGTAGCTCAGTTTGTAGAATGCTTGCATAGCATAAATGAAG  
TCCTGGGTTCCTATCCCCAGCACCACATAAATGCAGGTAAGAAACAGAGTCAGGAGGA  
CCAAGCATTCTCCTTGGCTACATAACAAAAGCAAGGCCTTTGTCCCCATGTCTTGGC  
TACAAGAGACCCTATCTCAGAAAATTGTGGGGGGGAGGGGGGGGGAAATGGCCTTGA  
AAACACAGCCAGTCACTGTCACTGCATTGCCAGAAGTGGTGGATCCCAGGTGTGCTT  
GGCAGATAACAGCTAAAAGGCACATAACCTTGGTGGGGAAATAAATGCCTGTGGTGT  
CCTGAGGGCCCCACCAAGTTCCAAAAAAAAAAAAA

>gi|18997007|gb|AAL83249.1|AF474154\_1 N-  
acetylglucosaminyltransferase V [Mus musculus]

MAFFSPWKLSSQKLGFVLVTFGFIWGMMLLHFTIQQRTQPESSSMLREQILDLSKRY  
IKALAEENRDVVDGPYAGVMTAYDLKKTALVLLDNILQIRIGKLESKVDNLVNGTGAN  
STNSTTAVPSLVLEKINVADIINGVQEKCVLPMDGYPHCEGKIKWMKDMWRS DPC  
YADYGVDGTSCSFFIYLSEVENWCPRLPWRAKNPYEEADHNSLAEIRTD FNI LYGMM  
KKHEEFRWMRLRIRRMADAWIQAIKSLAEKQNLKRKRKKILVHLGLLT KESGFKIA  
ETAFSGGPLGELVQWSDLITSLYLLGHDIRISASLAE LKEIMKKVVGNRSGCPTVGD  
RIVELIYIDIVGLAQFKKTLGPSWVHYQCMLRVLD SFGTEPEFNHAS YAQSKGHKTP  
WGKWNLNPPQQFYTMFPHTPDNSFLGFVVEQHLN SSDIHHINEIKRQNQSLVYGK VDS  
FWKNKKIYLDIIHTYMEVHATVYGSSTKNIPSYVKNHGILSGRDLQFL LRETKLFVG  
LGFPYEGPAPLEA IANGCAFLNPKFNPPKSSKNTDFFIGKPTLRELTSQH PYAEVFI  
GRPHVWTVDLNNREEVEDAVKAILNQKIEPYMPYEFTCEGMLQRINAFIEKQDFCHG  
QVMWPPLSALQVKLAEPGQSQCKQVCQESQLICEPSFFQHLNKEKDLLKYKVTCQSSE  
LYKDILVPSFYPKSKHCVFQGDLLLFSCAGAHPTHQRICPCRDFIKGQVALCKDCL

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